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From: Mertz, Prema
Sent: Thursday, March 02, 2006 2:44 PM
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Subject: 10/695,994

Please search any 6 amino acids of SEQ ID NO:7 with protein databases.

Thanks.

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Type of Search
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Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

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OM protein - protein search, using sw model

Run on: March 4, 2006, 07:02:06 ; Search time 187 Seconds
(without alignments)
516.916 Million cell updates/sec

Title: US-10-695-994A-7
Perfect score: 220
Sequence: 1 MEIQRITSSISGPISPAYTQ.....QNYKFNRSRRASDHSWSGM 220

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 6

Total number of hits satisfying chosen parameters: 4830

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: Geneseq.21:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	220	7	ADP74494
2	220	100.0	220	8	ADQ88366
3	129	58.6	220	2	AAW81640
4	124	56.4	1022	8	ADP13682
5	124	56.4	2154	2	AAW81639
6	124	56.4	2154	7	ADP74491
7	124	56.4	2154	9	ADQ88363
8	124	56.4	2154	9	ADZ85101
9	97	44.1	321	6	ABU70467
10	97	44.1	1630	7	ADU70517
11	97	44.1	2364	5	ABP70625
12	97	44.1	2364	8	ABM80299
13	97	44.1	2364	8	ADZ70337
14	97	44.1	2364	9	ADZ70337
15	90	40.9	1120	2	AAW81642
16	38	17.3	2106	7	ADJ70287
17	38	17.3	2137	9	ADX06608
18	38	17.3	2141	6	ABR41636
19	38	17.3	2387	2	AAU01183
20	27	12.3	2390	2	AAU05494
21	23	10.5	806	4	ABP41709
22	19	8.6	2291	4	ABB61876
23	15	6.8	15	7	ADP74518
24	15	6.8	15	8	ADQ88396

25	15	6.8	17	9	ADV13561
26	15	6.8	17	9	ADV13562
27	14	6.4	14	27	AAW81644
28	14	6.4	14	7	ADP74507
29	14	6.4	14	8	ADQ88379
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32	14	6.4	2326	8	ADN23721
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36	11	5.0	1092	3	AAV59237
37	11	5.0	1201	3	AAV59240
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49	11	5.0	5430	9	ADZ85102
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51	11	5.0	7201	4	ABW71136
52	10	4.5	5385	4	ABW66487
53	10	4.5	5496	4	ABW67161
54	9	4.1	67	5	ABP62976
55	9	4.1	72	2	AAW93379
56	9	4.1	108	3	AAW01083
57	9	4.1	117	4	ABG11927
58	9	4.1	201	1	ABP98499
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62	9	4.1	474	4	ABW67963
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66	9	4.1	2105	8	ADQ44170
67	9	4.1	3064	6	ABO14706
68	9	4.1	3215	8	ADN11060
69	9	4.1	3227	8	ADN11061
70	9	4.1	3432	9	ADW10726
71	9	4.1	3433	2	AAW22017
72	9	4.1	3433	7	ADJ68925
73	9	4.1	3433	8	ADJ68926
74	9	4.1	3433	8	ADP55624
75	9	4.1	4576	8	ADOS5184
76	9	4.1	236	6	ADY64900
77	8	3.6	358	6	ABJ25461
78	8	3.6	417	7	ABM84663
79	8	3.6	517	6	ABJ26061
80	8	3.6	547	4	ABW63123
81	8	3.6	592	8	ADN72217
82	8	3.6	626	6	ABR41653
83	8	3.6	690	4	ABW63142
84	8	3.6	884	5	ABG34125
85	8	3.6	894	8	ADL24315
86	8	3.6	894	8	ADX26296
87	8	3.6	894	9	ADX26371
88	8	3.6	911	7	ADW62304
89	8	3.6	911	7	ADW62302
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91	8	3.6	912	4	AAW90771
92	8	3.6	912	5	ABG34124
93	8	3.6	912	6	ABU89754
94	8	3.6	912	6	ADL24316
95	8	3.6	937	4	AAW63240
96	8	3.6	1190	8	ADN29513
97	8	3.6			

98	8	3.6	1519	4	ABB66635	Abb66635 Drosophi1	171	7	3.2	267	8	ADL91559	ADL91559 Human tmr
99	8	3.6	2129	4	ABG15478	Abg15478 Novel hum	172	7	3.2	271	8	ADM32828	Adm32828 Amino aci
100	8	3.6	2129	4	ABG20749	Abg20749 Novel hum	173	7	3.2	274	8	AAg06912	AAg06912 Arabidops
101	8	3.6	2414	2	AAW84882	Aaw84882 Transcrip	174	7	3.2	274	3	AAg53993	AAg53993 Arabidops
102	8	3.6	2414	2	AAW40057	Aaw40057 Cellular	175	7	3.2	280	8	ADX89926	Adx89926 Plant ful
103	8	3.6	2414	5	ABW06340	Abw06340 Human p30	176	7	3.2	291	2	ADT58314	Adt58314 Plant pol
104	8	3.6	2414	6	ABU03968	Abu03968 Human exp	177	7	3.2	295	2	AAW86128	Aaw86128 Human Mac
105	8	3.6	2414	6	ABU03980	Abu03980 Human exp	178	7	3.2	295	7	ADC39152	Adc39152 Novel hum
106	8	3.6	2414	6	ABU03975	Abu03975 Human exp	179	7	3.2	298	8	ADX78880	Adx78880 Plant ful
107	8	3.6	2414	6	ABU03978	Abu03978 Human exp	180	7	3.2	300	8	ADU01159	Adu01159 Human pro
108	8	3.6	2414	6	ABU03976	Abu03976 Human exp	181	7	3.2	300	8	ADU15541	Adu15541 Novel hum
109	8	3.6	4097	6	ABW57815	Abw57815 Drosophi1	182	7	3.2	302	9	ADM17390	Adm17390 Eucalyptu
110	8	3.6	4101	8	ADN23857	Adn23857 Bacteri1	183	7	3.2	306	4	ABG03251	ABG03251 Novel hum
111	8	3.6	4101	8	ADN23856	Adn23856 Bacteri1	184	7	3.2	306	5	ABP38671	ABP38671 Novel hum
112	7	3.2	9	4	AAE01104	Aae01104 Human leu	185	7	3.2	306	8	ADSO5186	Adso5186 Staphyloc
113	7	3.2	13	2	AAW81643	Aaw81643 Mouse elf	186	7	3.2	307	8	ADU02746	Adu02746 Novel hum
114	7	3.2	13	7	ADP74506	Adp74506 Peptide f	187	7	3.2	309	8	ADQ66295	Adq66295 Novel hum
115	7	3.2	13	8	ADQ88378	Adq88378 Mouse elf	188	7	3.2	314	3	AAW91560	AAW91560 Human sec
116	7	3.2	13	8	ADQ88395	Adq88395 Mouse elf	189	7	3.2	314	3	AAW91560	AAW91560 Human sec
117	7	3.2	32	7	ADQ06181	Adq06181 Yeast MAB	190	7	3.2	314	8	ADL71751	Adl71751 Novel hum
118	7	3.2	55	8	ABO56432	AbO56432 Human gen	191	7	3.2	314	8	ADL71635	Adl71635 Novel hum
119	7	3.2	67	4	AAU46339	Aau46339 Propionib	192	7	3.2	316	5	AAW42795	AAW42795 Streptoco
120	7	3.2	67	6	ABW42858	Abw42858 Propionib	193	7	3.2	316	5	ABP29264	ABP29264 M. xanthu
121	7	3.2	74	2	AAW33806	Aaw33806 YUL124C a	194	7	3.2	319	9	ABW95298	ABW95298 Human neu
122	7	3.2	91	7	ADJ70926	Adj70926 Human hea	195	7	3.2	321	6	ABR43288	ABR43288 Human neu
123	7	3.2	95	4	AAU48469	Aau48469 Propionib	196	7	3.2	326	2	AAW20109	AAW20109 B. burgdo
124	7	3.2	95	6	ABW44988	Abw44988 Propionib	197	7	3.2	329	6	ABD11406	ABD11406 Allotococ
125	7	3.2	100	6	ABW66150	Abw66150 Novel hum	198	7	3.2	344	4	ABW58880	ABW58880 Drosophi1
126	7	3.2	109	4	ABG26491	Abg26491 Novel hum	199	7	3.2	346	7	ADC39150	Adc39150 Novel hum
127	7	3.2	115	3	ABW58937	Abw58937 Breast an	200	7	3.2	347	2	AAW20108	AAW20108 B. burgdo
128	7	3.2	120	4	AAW18063	Aaw18063 Peptide #	201	7	3.2	352	7	ADC39146	Adc39146 Novel hum
129	7	3.2	120	4	ABW37101	Abw37101 Peptide #	202	7	3.2	352	7	ADQ66129	ADQ66129 Novel hum
130	7	3.2	120	4	AAW30575	Aaw30575 Peptide #	203	7	3.2	357	8	AAW53992	AAW53992 Arabidops
131	7	3.2	120	4	ABW31865	Abw31865 Peptide #	204	7	3.2	358	3	AAW06911	AAW06911 Arabidops
132	7	3.2	120	4	ABW22409	Abw22409 Protein #	205	7	3.2	358	5	ABW92618	ABW92618 Herbicida
133	7	3.2	120	4	AAW70237	Aaw70237 Human bra	206	7	3.2	358	5	AAW31707	AAW31707 Flavonone
134	7	3.2	120	4	AAW57823	Aaw57823 Human Dcn	207	7	3.2	358	6	AAW31707	AAW31707 Flavonone
135	7	3.2	120	4	AAW51934	Abw51934 Human liv	208	7	3.2	358	9	ADZ25324	ADZ25324 Human Mac
136	7	3.2	120	4	AAW05702	Aaw05702 Peptide #	209	7	3.2	360	2	AAW33492	AAW33492 Human neu
137	7	3.2	120	5	ABG39875	Abg39875 Human pep	210	7	3.2	362	6	ABR43289	ABR43289 Human neu
138	7	3.2	132	4	ABW11597	Abw11597 Human sec	211	7	3.2	365	6	ABG74623	ABG74623 Parsley F
139	7	3.2	132	6	ABW11665	Abw11665 Human MDD	212	7	3.2	366	6	ABW94255	ABW94255 Trifolium
140	7	3.2	140	8	ADW89759	Adw89759 Protein f	213	7	3.2	366	6	ABW94281	ABW94281 Trifolium
141	7	3.2	156	5	ABP51297	Abp51297 Human MDD	214	7	3.2	368	7	ADC39148	Adc39148 Novel hum
142	7	3.2	158	4	ABW53284	Abw53284 Human tes	215	7	3.2	373	3	ADQ26520	ADQ26520 Human ata
143	7	3.2	158	6	ADW10654	Adw10654 Allotococ	216	7	3.2	384	6	ABW70528	ABW70528 Human adi
144	7	3.2	158	7	ADW60213	Adw60213 Secreted	217	7	3.2	384	7	ABO75340	ABO75340 Pseudomon
145	7	3.2	160	7	ABO79500	AbO79500 Pseudomon	218	7	3.2	385	7	ADW59634	ADW59634 Pseudomon
146	7	3.2	166	3	AAW38862	Aaw38862 Arabidops	219	7	3.2	392	3	AAW29453	AAW29453 Arabidops
147	7	3.2	168	8	ADU02925	Adu02925 Novel hum	220	7	3.2	397	5	ABW48741	ABW48741 Bacteria1
148	7	3.2	172	6	ABW53405	Abw53405 Protein s	221	7	3.2	399	8	ADW24890	ADW24890 Bacteria1
149	7	3.2	172	6	ADW10652	Adw10652 Allotococ	222	7	3.2	401	7	ABO78163	ABO78163 Pseudomon
150	7	3.2	172	6	ADW64720	Adw64720 Disease t	223	7	3.2	412	3	AAW29452	AAW29452 Arabidops
151	7	3.2	173	8	ADW67034	Adw67034 Novel hum	224	7	3.2	422	6	ABW25881	ABW25881 Aspergill
152	7	3.2	186	7	ADW65572	Adw65572 Human pro	225	7	3.2	426	6	ABW26481	ABW26481 Aspergill
153	7	3.2	186	8	ADW58909	Adw58909 Human Elk	226	7	3.2	426	6	ADW11404	ADW11404 Allotococ
154	7	3.2	199	7	ADW05425	Adw05425 Human pro	227	7	3.2	433	6	AAW30802	AAW30802 Human SH2
155	7	3.2	205	8	ADW14070	Adw14070 Human bar	228	7	3.2	438	7	ABO68604	ABO68604 Pseudomon
156	7	3.2	211	4	AAW01083	Aaw01083 Human col	229	7	3.2	450	8	ADW06447	ADW06447 B. lichen
157	7	3.2	211	7	ABW88336	Abw88336 Rice abio	230	7	3.2	450	8	ADW34526	ADW34526 POSH prot
158	7	3.2	212	4	AAW63593	Aaw63593 Human gas	231	7	3.2	451	7	ABO78856	ABO78856 Pseudomon
159	7	3.2	218	5	ABW51582	Abw51582 Purine/py	232	7	3.2	453	6	ABW25446	ABW25446 Protein e
160	7	3.2	218	8	ABO58433	AbO58433 Human gen	233	7	3.2	454	4	ABW22866	ABW22866 Novel hum
161	7	3.2	218	8	ADW29497	Adw29497 Bacteria1	234	7	3.2	456	4	AAW40115	AAW40115 Human pol
162	7	3.2	221	4	AAW63595	Aaw63595 Human gas	235	7	3.2	465	4	AAW41901	AAW41901 Human pol
163	7	3.2	229	8	ADW15444	Adw15444 Rhodococ	236	7	3.2	470	8	ADW49948	ADW49948 Oll--aseoc
164	7	3.2	246	8	ADW2785	Adw2785 Plant ful	237	7	3.2	471	8	ADW020174	ADW020174 Human pro
165	7	3.2	253	8	ADW21602	Adw21602 Bacteria1	238	7	3.2	471	8	ADW25221	ADW25221 PRO polyp
166	7	3.2	254	3	AAW53994	AAW53994 Arabidops	239	7	3.2	471	1	AAW17776	AAW17776 PRO polyp
167	7	3.2	254	3	AAW06913	AAW06913 Arabidops	240	7	3.2	491	9	AAW70464	AAW70464 Sequence
168	7	3.2	258	3	AAW29454	AAW29454 Arabidops	241	7	3.2	498	9	ADW39495	ADW39495 HIV Gag p
169	7	3.2	259	3	AAW56375	Aaw56375 Human pro	242	7	3.2	500	5	ABP73751	ABP73751 Candida a
170	7	3.2	262	7	ADW60612	Adw60612 Human con	243	7	3.2	505	7	ADW48723	ADW48723 Human pro

244	7	3.2	524	5	ABP51657	Abp51657 Drosophila	317	7	3.2	956	7	ADM04352	Adm04352 Human pro
245	7	3.2	534	4	ABP93950	Abp93950 Human pro	318	7	3.2	957	4	AAW79016	AAW79016 Human pro
246	7	3.2	539	7	ADP08421	ADP08421 Novel pro	319	7	3.2	959	4	AAW41353	AAW41353 Human pol
247	7	3.2	540	4	AG74992	Ag74992 Human col	320	7	3.2	1002	4	AAW39567	AAW39567 Human pol
248	7	3.2	548	8	ADN17887	Adn17887 Bacterial	321	7	3.2	1002	9	ABE56484	ABE56484 Radiochem
249	7	3.2	549	7	ADP65325	Adp65325 Human pro	322	7	3.2	1002	9	ABE56484	ABE56484 Radiochem
250	7	3.2	555	7	ADP55438	Adp55438 Human nov	323	7	3.2	1045	6	ABU08495	ABU08495 Fruit fly
251	7	3.2	561	8	ADP86425	Adp86425 Aspergill	324	7	3.2	1074	6	ADJ50367	ADJ50367 Oil-aseoc
252	7	3.2	566	8	ADP66691	Adp66691 Novel hum	325	7	3.2	1091	6	ABU46052	ABU46052 Protein e
253	7	3.2	568	4	AAW40873	AAW40873 Human pol	326	7	3.2	1091	6	ADK47308	ADK47308 Streptoco
254	7	3.2	594	9	AEA25863	Aea25863 C. elegan	327	7	3.2	1100	3	AAW81511	AAW81511 Streptoco
255	7	3.2	595	4	AAU36514	AAU36514 Pseudomon	328	7	3.2	1100	4	AAW93286	AAW93286 Human pro
256	7	3.2	595	6	ABU38917	Abu38917 Protein e	329	7	3.2	1100	6	ABU01574	ABU01574 S. pneumo
257	7	3.2	597	8	ADN20612	Adn20612 Bacterial	330	7	3.2	1100	6	AAO29563	AAO29563 Human pro
258	7	3.2	602	3	AAW69204	AAW69204 Amino aci	331	7	3.2	1100	9	ADY70491	ADY70491 Human bet
259	7	3.2	603	6	ABO53099	AbO53099 Human put	332	7	3.2	1102	8	ADR96224	ADR96224 Novel S.
260	7	3.2	609	5	ABU65102	Abu65102 Human NOV	333	7	3.2	1102	9	AEA60094	AEA60094 Streptoco
261	7	3.2	609	8	ADN61855	Adn61855 Human nov	334	7	3.2	1106	7	ADP46435	ADP46435 Rat Prote
262	7	3.2	611	4	AAW80000	AAW80000 Human pro	335	7	3.2	1146	7	ADP50150	ADP50150 Murine de
263	7	3.2	621	4	AAW80000	AAW80000 Human pro	336	7	3.2	1147	9	ADW71979	ADW71979 Murine DI
264	7	3.2	628	8	ADP08839	Adp08839 Human DAN	337	7	3.2	1150	5	AAW40294	AAW40294 Human pol
265	7	3.2	639	3	AAW51038	AAW51038 Human pro	338	7	3.2	1150	5	ABG32465	ABG32465 Human pro
266	7	3.2	639	4	AAW78485	AAW78485 Human pro	339	7	3.2	1150	7	ADP50152	ADP50152 Human pro
267	7	3.2	642	3	ABP64400	Abp64400 Human ORF	340	7	3.2	1150	8	ADP50152	ADP50152 Human pro
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269	7	3.2	649	8	ADP24693	Adp24693 Bacterial	342	7	3.2	1150	9	ADY91605	ADY91605 Human pro
270	7	3.2	656	2	AAW04627	AAW04627 Mouse rec	343	7	3.2	1151	9	ADW71952	ADW71952 Murine DI
271	7	3.2	656	2	AAW80994	AAW80994 Human rec	344	7	3.2	1161	9	ADW83142	ADW83142 Murine in
272	7	3.2	657	8	ADJ71949	Adj71949 Human PPM	345	7	3.2	1162	6	ADW5137	ADW5137 Human pro
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276	7	3.2	669	6	ABU39755	Abu39755 Protein e	349	7	3.2	1227	7	ADP71295	ADP71295 Novel hum
277	7	3.2	673	7	ABD64271	ABD64271 Human pro	350	7	3.2	1253	6	AAW98821	AAW98821 Human str
278	7	3.2	673	7	ABO75176	ABO75176 Pseudomon	351	7	3.2	1253	6	AAW78455	AAW78455 Human pro
279	7	3.2	678	4	AAW79469	AAW79469 Human pro	352	7	3.2	1265	5	ABE57282	ABE57282 Mouse isc
280	7	3.2	685	6	ABR41545	ABr41545 Human.DIT	353	7	3.2	1265	8	ADP00098	ADP00098 Mouse hom
281	7	3.2	686	8	ABM84061	ABm84061 Human dia	354	7	3.2	1282	8	ADP21864	ADP21864 Human ves
282	7	3.2	698	3	AAV91524	AAV91524 Human sec	355	7	3.2	1285	6	ABR47540	ABR47540 Breast ca
283	7	3.2	698	4	AAW93431	AAW93431 Human pol	356	7	3.2	1285	7	ADP75449	ADP75449 Prostata
284	7	3.2	698	8	ADL71596	Adl71596 Novel hum	357	7	3.2	1285	8	ADL12778	ADL12778 Human ste
285	7	3.2	698	8	ADL10372	Adl10372 Human pro	358	7	3.2	1285	8	ADP00098	ADP00098 Human hom
286	7	3.2	698	8	ADL10372	Adl10372 Human pro	359	7	3.2	1285	9	ADW71980	ADW71980 Human DIS
287	7	3.2	698	8	ABM80566	ABm80566 Tumour-as	360	7	3.2	1289	9	ADW71978	ADW71978 Murine DI
288	7	3.2	699	9	ADP85513	ADp85513 Human tra	361	7	3.2	1299	3	AAW58633	AAW58633 Protein r
289	7	3.2	701	6	ABU38904	ABu38904 Protein e	362	7	3.2	1299	4	AAW78454	AAW78454 Human pro
290	7	3.2	701	6	ABU41400	ABu41400 Protein e	363	7	3.2	1299	4	ADZ09816	ADZ09816 Human bre
291	7	3.2	702	8	ADN21371	Adn21371 Bacterial	364	7	3.2	1307	4	AAW79438	AAW79438 Human pro
292	7	3.2	702	8	ADN21371	Adn21371 Bacterial	365	7	3.2	1307	4	AAW79438	AAW79438 Human pro
293	7	3.2	703	7	ABO75159	ABO75159 Pseudomon	366	7	3.2	1311	6	ADP10025	ADP10025 Allicococ
294	7	3.2	705	8	ADJ50107	Adj50107 Oil-aseoc	367	7	3.2	1315	9	ADP06797	ADP06797 CycLin-de
295	7	3.2	717	8	ADN21501	ADn21501 Bacterial	368	7	3.2	1319	9	ADP06797	ADP06797 CycLin-de
296	7	3.2	718	4	AAW92973	AAW92973 Human pro	369	7	3.2	1336	6	ABR52816	ABR52816 Protein e
297	7	3.2	718	8	ADP88419	ADp88419 Human pro	370	7	3.2	1336	6	ADK62224	ADK62224 Disease t
298	7	3.2	721	9	ADZ26477	Adz26477 Human ery	371	7	3.2	1336	8	ADN19070	ADN19070 Bacterial
299	7	3.2	730	5	ABR98317	ABr98317 Human leu	372	7	3.2	1383	6	ADP10023	ADP10023 Allicococ
300	7	3.2	731	7	ABG17452	ABg17452 Novel hum	373	7	3.2	1443	6	ABG74688	ABG74688 Human GGD
301	7	3.2	731	7	ADM03766	Adm03766 Human pro	374	7	3.2	1584	8	ABW80133	ABW80133 Tumour-as
302	7	3.2	731	8	ADP34515	ADp34515 POSH prot	375	7	3.2	1644	7	ADJ69113	ADJ69113 Human hea
303	7	3.2	743	5	ADQ67542	Adq67542 Novel hum	376	7	3.2	1898	2	AAV30795	AAV30795 A human c
304	7	3.2	764	5	ADL17007	ADl17007 Bovine NO	377	7	3.2	1898	7	ADP48869	ADP48869 Human pro
305	7	3.2	798	4	AAW93238	AAW93238 Human pro	378	7	3.2	1902	6	ABJ38695	ABJ38695 Human nuc
306	7	3.2	805	7	ABO70119	ABO70119 Pseudomon	379	7	3.2	2000	8	ADN03898	ADN03898 Antipsoi
307	7	3.2	857	8	ADX76173	ADx76173 Plant ful	380	7	3.2	2000	8	ADP25346	ADP25346 PRO polyp
308	7	3.2	861	4	ABW63028	ABW63028 Drosophi	381	7	3.2	2285	9	ADW02024	ADW02024 Human MPT
309	7	3.2	871	4	ABW58282	ABW58282 Drosophi	382	7	3.2	2285	9	ABW58282	ABW58282 Human MPT
310	7	3.2	871	5	AAW48928	AAW48928 Thermophi	383	7	3.2	2441	2	AAW79054	AAW79054 CREB bind
311	7	3.2	871	5	AAW48927	AAW48927 Thermophi	384	7	3.2	2441	2	AAW40058	AAW40058 CREB bind
312	7	3.2	876	9	AEA25861	Aea25861 C. elegan	385	7	3.2	2441	3	AAW94252	AAW94252 Mouse nuc
313	7	3.2	876	9	AEA25890	Aea25890 C. elegan	386	7	3.2	2441	4	ABW44555	ABW44555 Mouse wou
314	7	3.2	878	7	ADP74139	ADp74139 Human nov	387	7	3.2	2441	6	ABU03977	ABU03977 Human exp
315	7	3.2	900	7	ADJ69696	ADj69696 Human hea	388	7	3.2	2441	8	ADP90352	ADP90352 Mouse CRE
316	7	3.2	916	8	ADR89554	ADR89554 Oysterol	389	7	3.2	2441	8	ADR87292	ADR87292 Mouse CRE

536	6	2.7	56	4	ABB17456	Abb17456 Human ner	609	6	2.7	75	4	AAW34055	Aam34055 Peptide #
537	6	2.7	56	5	ABG36709	Abg36709 Human pep	610	6	2.7	75	4	ABR24739	Abb24739 Protein #
538	6	2.7	57	3	AAAG59934	Aag59934 Arabidops	611	6	2.7	75	4	AAW73873	Aam73873 Human bon
539	6	2.7	58	4	AAU60632	Aau60632 Propionib	612	6	2.7	75	4	AAW61159	Aam61159 Human bra
540	6	2.7	58	4	AAU63534	Aau63534 Propionib	613	6	2.7	75	4	ABG55624	Abg55624 Human liv
541	6	2.7	58	6	ABM60053	Abm60053 Propionib	614	6	2.7	75	5	ABG43761	Abg43761 Human pep
542	6	2.7	58	6	ABM65854	Abm65854 Propionib	615	6	2.7	76	3	AAAG55742	Aag555742 Arabidops
543	6	2.7	58	6	ABM57151	Abm57151 Propionib	616	6	2.7	76	3	AAAG60173	Aag60173 Arabidops
544	6	2.7	59	4	AAAG92798	AAg92798 C glutami	617	6	2.7	76	3	AAAG58776	Aag58776 Arabidops
545	6	2.7	59	4	ABG03925	Abg03925 Novel hum	618	6	2.7	76	3	AAAG55353	Aag55353 Arabidops
546	6	2.7	60	3	AAAG15603	Aag15603 Arabidops	619	6	2.7	77	4	AAW91396	AAw91396 Human imm
547	6	2.7	60	4	AAU50590	Aau50590 Propionib	620	6	2.7	77	4	ABO80837	ABO80837 Pseudomon
548	6	2.7	60	4	AAU46529	Aau46529 Propionib	621	6	2.7	78	2	AAAL5744	AAAL5744 R18 antiig
549	6	2.7	60	4	ABG20913	Abg20913 Novel hum	622	6	2.7	78	2	AAW99828	AAw99828 HIV HBX2
550	6	2.7	60	6	ABM43048	Abm43048 Propionib	623	6	2.7	78	4	AAW85995	AAw85995 Amino aci
551	6	2.7	60	6	ABM47419	Abm47419 Propionib	624	6	2.7	78	6	AAO30521	AAO30521 HIV vpr m
552	6	2.7	60	7	ABR42471	Abt42471 HIV viral	625	6	2.7	78	6	AAO30515	AAO30515 HIV vpr n
553	6	2.7	61	4	AAU41928	Aau41928 Propionib	626	6	2.7	78	6	AAO30516	AAO30516 HIV vpr m
554	6	2.7	61	6	ABM38447	Abm38447 Propionib	627	6	2.7	78	6	AAO30519	AAO30519 HIV vpr m
555	6	2.7	61	7	ADD35689	Add35689 Human hep	628	6	2.7	78	6	AAO30517	AAO30517 HIV vpr m
556	6	2.7	62	6	ADP36270	Adp36270 Actinoba	629	6	2.7	78	6	AAO30518	AAO30518 HIV vpr m
557	6	2.7	62	8	ADP07828	Adp07828 Human sec	630	6	2.7	78	6	AAO30520	AAO30520 HIV vpr m
558	6	2.7	63	4	AAU56121	Aau56121 Propionib	631	6	2.7	78	8	ADN36417	ADN36417 HIV vpr m
559	6	2.7	63	4	AAU49893	Aau49893 Propionib	632	6	2.7	78	8	ADX96214	ADx96214 Plant ful
560	6	2.7	63	6	ABM46412	Abm46412 Propionib	633	6	2.7	79	2	AAAL8961	AAAL8961 NL4-3 VPR
561	6	2.7	63	6	ABM52640	Abm52640 Propionib	634	6	2.7	80	7	ABO60704	ABO60704 Klebsiell
562	6	2.7	64	4	AAU53994	Aau53994 Propionib	635	6	2.7	80	7	ADL27014	ADL27014 Human 339
563	6	2.7	64	6	ABM50513	Abm50513 Propionib	636	6	2.7	81	4	AAU86504	AAU86504 Novel hum
564	6	2.7	65	4	AAU61820	Aau61820 Propionib	637	6	2.7	81	4	AAU50363	AAU50363 Propionib
565	6	2.7	65	4	ABG06896	Abg06896 Novel hum	638	6	2.7	81	5	ABP31762	ABP31762 Human ORF
566	6	2.7	65	6	ABM57739	Abm57739 Propionib	639	6	2.7	81	6	ABM46882	ABM46882 Propionib
567	6	2.7	65	6	ABM71604	Abm71604 Staphyloc	640	6	2.7	81	7	ADBS9838	ADBS9838 Connectiv
568	6	2.7	66	4	AAU66720	Aau66720 Propionib	641	6	2.7	82	4	AAW83284	AAW83284 Human imm
569	6	2.7	66	4	AAU52198	Aau52198 Propionib	642	6	2.7	82	4	AAU41336	AAU41336 Propionib
570	6	2.7	66	5	ABU60952	Abu60952 Lung spec	643	6	2.7	82	6	ABM37855	ABM37855 Propionib
571	6	2.7	66	5	ADP94731	Adp94731 Hepatit	644	6	2.7	83	4	AAU46839	AAU46839 Propionib
572	6	2.7	66	6	ABM48717	Abm48717 Propionib	645	6	2.7	83	4	AAU66297	AAU66297 Propionib
573	6	2.7	66	6	ABM63239	Abm63239 Propionib	646	6	2.7	83	5	ABP42262	ABP42262 Human ova
574	6	2.7	66	7	ADP07640	Adp07640 Bacterial	647	6	2.7	83	5	ABM43358	ABM43358 Propionib
575	6	2.7	67	4	AAW13788	Aaw13788 Peptide #	648	6	2.7	83	6	ABW62816	ABW62816 Propionib
576	6	2.7	67	4	ABW68657	Abw68657 Drosophi	649	6	2.7	83	9	ADX40859	ADx40859 HIV vpr p
577	6	2.7	67	4	ABW41378	Abw41378 Peptide #	650	6	2.7	84	2	AAW95979	AAW95979 Nucleic a
578	6	2.7	67	4	ABW32722	Abw32722 Peptide #	651	6	2.7	84	5	AAW52410	AAW52410 Protease
579	6	2.7	67	4	AAW26186	Aaw26186 Peptide #	652	6	2.7	85	3	AAW64719	AAW64719 Human 5'
580	6	2.7	67	4	AAW35168	Aaw35168 Peptide #	653	6	2.7	85	3	AAW00616	AAW00616 Human sec
581	6	2.7	67	4	ABW27563	Abw27563 Human pep	654	6	2.7	85	4	ABG05351	ABG05351 Novel hum
582	6	2.7	67	4	ABW18208	Abw18208 Protein #	655	6	2.7	85	5	ABW10002	ABW10002 Human pro
583	6	2.7	67	4	ABW25308	Abw25308 Protein #	656	6	2.7	85	5	ABW10017	ABW10017 Human rep
584	6	2.7	67	4	AAW75051	Aaw75051 Human bon	657	6	2.7	85	5	ABW64636	ABW64636 Human alb
585	6	2.7	67	4	AAW53540	Aaw53540 Human bra	658	6	2.7	85	5	ABW64638	ABW64638 Human alb
586	6	2.7	67	4	AAW62247	Aaw62247 Human bra	659	6	2.7	85	8	ADL77903	ADL77903 Albumin f
587	6	2.7	67	4	ABW47577	Abw47577 Human liv	660	6	2.7	85	8	ADU77905	ADU77905 Albumin f
588	6	2.7	67	4	ABW56816	Abw56816 Human liv	661	6	2.7	85	9	ADZ73283	ADz73283 Signal pe
589	6	2.7	67	4	AAW01533	AAW01533 Peptide #	662	6	2.7	85	9	ADZ73274	ADz73274 Human inc
590	6	2.7	67	5	ABG44757	Abg44757 Human pep	663	6	2.7	86	6	ABU11767	ABU11767 Human MDD
591	6	2.7	68	5	ABG35557	Abg35557 Human pep	664	6	2.7	87	4	AAW89216	AAW89216 Human imm
592	6	2.7	68	7	ABO66527	ABO66527 Klebsiell	665	6	2.7	88	2	AAW35878	AAW35878 Amino aci
593	6	2.7	69	6	ABP75975	ABP75975 Human GEN	666	6	2.7	88	3	AAW44944	AAW44944 Zea may
594	6	2.7	69	6	ABP76141	ABP76141 Human GEN	667	6	2.7	88	4	AAW95468	AAW95468 Human rep
595	6	2.7	70	4	AAAG75057	AAg75057 Human col	668	6	2.7	88	4	AAU45755	AAU45755 Propionib
596	6	2.7	70	8	ABO54240	ABO54240 Human gen	669	6	2.7	88	4	ABW96153	ABW96153 Human tes
597	6	2.7	71	4	AAW87393	AAW87393 Human imm	670	6	2.7	88	5	ABP11139	ABP11139 Human ORF
598	6	2.7	71	4	AAW90859	AAW90859 Human imm	671	6	2.7	88	6	ABW42274	ABW42274 Propionib
599	6	2.7	72	2	AAW94547	AAW94547 Fragment	672	6	2.7	89	4	ABW68584	ABW68584 Drosophi
600	6	2.7	72	3	AAW53250	AAW53250 SIV Vpr p	673	6	2.7	90	3	AAW44943	AAW44943 Zea may
601	6	2.7	72	3	AAW61246	AAW61246 Arabidops	674	6	2.7	90	4	AAU50500	AAU50500 Propionib
602	6	2.7	72	3	AAW55704	AAW55704 Arabidops	675	6	2.7	90	5	ABP04104	ABP04104 Human ORF
603	6	2.7	72	3	AAW54445	AAW54445 Propionib	676	6	2.7	90	6	ABW08575	ABW08575 Human ORF
604	6	2.7	72	6	ABW50864	ABW50864 Propionib	677	6	2.7	90	6	ABW47019	ABW47019 Propionib
605	6	2.7	73	3	AAW44945	AAW44945 Zea may	678	6	2.7	91	3	AAW56564	AAW56564 C. eleg
606	6	2.7	74	4	ABW67692	ABW67692 Drosophi	679	6	2.7	91	4	ABW41436	ABW41436 Peptide #
607	6	2.7	75	4	AAW20135	AAW20135 Peptide #	680	6	2.7	91	4	AAW35228	AAW35228 Peptide #
608	6	2.7	75	4	ABW40351	ABW40351 Peptide #	681	6	2.7	91	4	ABW25336	ABW25336 Protein #

682	6	2.7	91	4	AAW75112	Human bon
683	6	2.7	91	4	AAW62309	Human bra
684	6	2.7	91	4	ABG56875	Human liv
685	6	2.7	91	5	ABG44796	Human pep
686	6	2.7	91	5	ADK40868	HIV Vpr p
687	6	2.7	92	3	AAW69305	HIV-1 non
688	6	2.7	92	4	ABG27173	Novel hum
689	6	2.7	92	4	ABG11873	Novel hum
690	6	2.7	92	5	ABP33004	Human ORF
691	6	2.7	93	3	AAW40589	Human ORF
692	6	2.7	93	3	ABG02968	Novel hum
693	6	2.7	93	4	ABG04388	Novel hum
694	6	2.7	93	4	ABG26512	Novel hum
695	6	2.7	94	5	ABW48618	Novel hum
696	6	2.7	94	8	ADL90099	Glycoprot
697	6	2.7	95	3	AAW69311	HIV-1 non
698	6	2.7	95	3	AAW69307	HIV-1 non
699	6	2.7	95	3	AAW57319	Propionib
700	6	2.7	95	6	ABW53838	Propionib
701	6	2.7	95	6	ADL78234	Endometxi
702	6	2.7	95	8	ADL05114	M. catarr
703	6	2.7	95	9	ADK40878	HIV Vpr p
704	6	2.7	95	9	ADK40850	HIV Vpr p
705	6	2.7	96	1	AAW81863	Sequence
706	6	2.7	96	1	AAW12258	HIV-1 str
707	6	2.7	96	2	AAW48963	HIV VPR.
708	6	2.7	96	2	AAW94544	Native VP
709	6	2.7	96	2	AAW53040	HIV-1 pol
710	6	2.7	96	2	AAW72395	HIV-1 pol
711	6	2.7	96	2	AAW29070	T. gondii
712	6	2.7	96	2	AAW99823	HIV L685
713	6	2.7	96	2	AAW99824	HIV H71C
714	6	2.7	96	2	AAW99821	HIV L64S
715	6	2.7	96	2	AAW99818	HIV A30S
716	6	2.7	96	2	AAW99826	HIV C75A
717	6	2.7	96	2	AAW99812	HIV-1 Vpr
718	6	2.7	96	2	AAW99819	HIV A30L
719	6	2.7	96	2	AAW99820	HIV A59P
720	6	2.7	96	2	AAW99825	HIV H71Y
721	6	2.7	96	2	AAW99827	HIV C76S
722	6	2.7	96	2	AAW99815	HIV Vpr w
723	6	2.7	96	2	AAW99829	HIV Vpr p
724	6	2.7	96	2	AAW99822	HIV L67S
725	6	2.7	96	2	AAW99831	HIV B21.2
726	6	2.7	96	2	AAW27492	E. coli b
727	6	2.7	96	2	AAW27492	E. coli b
728	6	2.7	96	3	AAW10049	HIV-1 Vpr
729	6	2.7	96	3	AAW69303	HIV-1 non
730	6	2.7	96	3	AAW69306	HIV-1 non
731	6	2.7	96	3	AAW69304	HIV-1 non
732	6	2.7	96	3	AAW69302	HIV-1 reg
733	6	2.7	96	3	AAW10685	HIV-1 reg
734	6	2.7	96	3	AAW53247	HIV-1 LAI
735	6	2.7	96	5	AAW25541	T. gondii
736	6	2.7	96	5	AAW16129	Human imm
737	6	2.7	96	5	ABP56175	HIV-1 vir
738	6	2.7	96	5	AAW80187	HIV-1 Vpr
739	6	2.7	96	6	ABW55491	Amino aci
740	6	2.7	96	7	ADL01277	HIV-1 Vpr
741	6	2.7	96	7	ADG17316	T. gondii
742	6	2.7	96	8	ADL6812	HIV-1 Vpr
743	6	2.7	96	8	ABW79669	HIV-1 Vpr
744	6	2.7	96	8	ADL05255	HIV-1 reg
745	6	2.7	96	8	ADP20078	Human imm
746	6	2.7	96	8	ADP20070	Human imm
747	6	2.7	96	9	ADV23774	HIV-1 full
748	6	2.7	96	9	ADK40841	HIV Vpr p
749	6	2.7	96	9	ADK40869	HIV Vpr p
750	6	2.7	96	9	ADK40849	HIV Vpr p
751	6	2.7	96	9	ADK40845	HIV Vpr p
752	6	2.7	96	9	ADK40847	HIV Vpr p
753	6	2.7	96	9	ADK40848	HIV Vpr p
754	6	2.7	96	9	ADK40854	HIV Vpr p
755	6	2.7	96	9	ADK40864	HIV Vpr p
756	6	2.7	96	9	ADK40865	HIV Vpr p
757	6	2.7	96	9	ADK40884	HIV Vpr p
758	6	2.7	96	9	ADK40853	HIV Vpr p
759	6	2.7	96	9	ADK40877	HIV Vpr p
760	6	2.7	96	9	ADK40877	HIV Vpr p
761	6	2.7	96	9	ADK40844	HIV Vpr p
762	6	2.7	96	9	ADK40873	HIV Vpr p
763	6	2.7	96	9	ADK40881	HIV Vpr p
764	6	2.7	96	9	ADK40885	HIV Vpr p
765	6	2.7	96	9	ADK40874	HIV Vpr p
766	6	2.7	96	9	ADK40874	HIV Vpr p
767	6	2.7	96	9	ADK40874	HIV Vpr p
768	6	2.7	96	9	ADK40874	HIV Vpr p
769	6	2.7	96	9	ADK40874	HIV Vpr p
770	6	2.7	96	9	ADK40874	HIV Vpr p
771	6	2.7	96	9	ADK40874	HIV Vpr p
772	6	2.7	96	9	ADK40874	HIV Vpr p
773	6	2.7	96	9	ADK40874	HIV Vpr p
774	6	2.7	96	9	ADK40874	HIV Vpr p
775	6	2.7	96	9	ADK40874	HIV Vpr p
776	6	2.7	96	9	ADK40874	HIV Vpr p
777	6	2.7	96	9	ADK40874	HIV Vpr p
778	6	2.7	96	9	ADK40874	HIV Vpr p
779	6	2.7	96	9	ADK40874	HIV Vpr p
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781	6	2.7	96	9	ADK40874	HIV Vpr p
782	6	2.7	96	9	ADK40874	HIV Vpr p
783	6	2.7	96	9	ADK40874	HIV Vpr p
784	6	2.7	96	9	ADK40874	HIV Vpr p
785	6	2.7	96	9	ADK40874	HIV Vpr p
786	6	2.7	96	9	ADK40874	HIV Vpr p
787	6	2.7	96	9	ADK40874	HIV Vpr p
788	6	2.7	96	9	ADK40874	HIV Vpr p
789	6	2.7	96	9	ADK40874	HIV Vpr p
790	6	2.7	96	9	ADK40874	HIV Vpr p
791	6	2.7	96	9	ADK40874	HIV Vpr p
792	6	2.7	96	9	ADK40874	HIV Vpr p
793	6	2.7	96	9	ADK40874	HIV Vpr p
794	6	2.7	96	9	ADK40874	HIV Vpr p
795	6	2.7	96	9	ADK40874	HIV Vpr p
796	6	2.7	96	9	ADK40874	HIV Vpr p
797	6	2.7	96	9	ADK40874	HIV Vpr p
798	6	2.7	96	9	ADK40874	HIV Vpr p
799	6	2.7	96	9	ADK40874	HIV Vpr p
800	6	2.7	96	9	ADK40874	HIV Vpr p
801	6	2.7	96	9	ADK40874	HIV Vpr p
802	6	2.7	96	9	ADK40874	HIV Vpr p
803	6	2.7	96	9	ADK40874	HIV Vpr p
804	6	2.7	96	9	ADK40874	HIV Vpr p
805	6	2.7	96	9	ADK40874	HIV Vpr p
806	6	2.7	96	9	ADK40874	HIV Vpr p
807	6	2.7	96	9	ADK40874	HIV Vpr p
808	6	2.7	96	9	ADK40874	HIV Vpr p
809	6	2.7	96	9	ADK40874	HIV Vpr p
810	6	2.7	96	9	ADK40874	HIV Vpr p
811	6	2.7	96	9	ADK40874	HIV Vpr p
812	6	2.7	96	9	ADK40874	HIV Vpr p
813	6	2.7	96	9	ADK40874	HIV Vpr p
814	6	2.7	96	9	ADK40874	HIV Vpr p
815	6	2.7	96	9	ADK40874	HIV Vpr p
816	6	2.7	96	9	ADK40874	HIV Vpr p
817	6	2.7	96	9	ADK40874	HIV Vpr p
818	6	2.7	96	9	ADK40874	HIV Vpr p
819	6	2.7	96	9	ADK40874	HIV Vpr p
820	6	2.7	96	9	ADK40874	HIV Vpr p
821	6	2.7	96	9	ADK40874	HIV Vpr p
822	6	2.7	96	9	ADK40874	HIV Vpr p
823	6	2.7	96	9	ADK40874	HIV Vpr p
824	6	2.7	96	9	ADK40874	HIV Vpr p
825	6	2.7	96	9	ADK40874	HIV Vpr p
826	6	2.7	96	9	ADK40874	HIV Vpr p
827	6	2.7	96	9	ADK40874	HIV Vpr p

828	2.7	110	4	AAM90884	Human	Imm	901	2.7	125	4	ABB20920	Abb20920	Protein #
829	2.7	110	5	AAB65119	Human	NP	902	2.7	125	4	AA668679	Aam66879	Human bon
830	2.7	110	5	ABP09182	Human	ORF	903	2.7	125	4	AA565301	Aam56301	Human bra
831	2.7	111	2	ADY37612	Lung	canc	904	2.7	125	4	ABG50343	Abg50343	Human liv
832	2.7	111	2	AAW38667	Streptoco		905	2.7	125	4	AAW04220	Aam04220	Human
833	2.7	111	4	AAW84540	Human	Imm	906	2.7	125	5	ABG38258	Abg38258	Human pep
834	2.7	111	4	AAU48005	Propionib		907	2.7	126	3	AAAG4910	Aag4910	Zea maye
835	2.7	111	6	ABW44524	Propionib		908	2.7	126	4	AAW79706	Aaw79706	Coryneb
836	2.7	112	8	ADN17279	Arabidops		909	2.7	126	7	ABO72980	AbO72980	Pseudom
837	2.7	112	8	ADR16842	Arabidops		910	2.7	127	4	ABG20770	AbG20770	Novel hum
838	2.7	112	9	ADV66224	Arabidops		911	2.7	127	8	ADSI1507	AdSI1507	Pseudom
839	2.7	113	3	AAW25179	Eucalyptu		912	2.7	127	8	ADX95363	AdX95363	Plant ful
840	2.7	113	4	AAU52411	Propionib		913	2.7	128	2	AAW88539	Aaw88539	Secreted
841	2.7	113	6	ABW48930	Propionib		914	2.7	128	4	ABW50306	AbW50306	Human sec
842	2.7	113	6	ABU43568	Propionib		915	2.7	128	5	ADK35127	AdK35127	Novel hum
843	2.7	113	6	ABU42565	Protein e		916	2.7	128	6	ABO44563	AbO44563	Novel hum
844	2.7	113	6	ABU16015	Protein e		917	2.7	128	7	ABO26043	AbO26043	Human pro
845	2.7	113	7	ADD12429	PDZ	ligan	918	2.7	129	4	AAW75924	Aaw75924	Human pol
846	2.7	113	8	AD153451	Human	PDZ	919	2.7	129	4	AAO01201	Aao01201	Human pol
847	2.7	113	8	ADM33542	Human	PDZ	920	2.7	129	7	ADC37544	AdC37544	Human nuc
848	2.7	113	8	ADO20973	PDZ	domai	921	2.7	129	8	ADX96651	AdX96651	Plant ful
849	2.7	113	8	ADR82914	PDZ	domai	922	2.7	130	2	AAV42116	Aay42116	Soybean a
850	2.7	113	8	ADU15906	Human	KIA	923	2.7	130	4	AAO05077	Aao05077	Human pol
851	2.7	113	8	ADU67331	Human	KIA	924	2.7	130	4	AAU30652	Aau30652	Novel hum
852	2.7	113	9	ADW52545	Human	PDZ	925	2.7	130	5	ABR40527	AbR40527	Human sec
853	2.7	113	9	AEB07696	Human	PDZ	926	2.7	130	5	ABR40448	AbR40448	Human sec
854	2.7	113	9	AER98710	Human	PDZ	927	2.7	131	3	AAAG10065	Aag10065	Arabidops
855	2.7	114	4	ABBI2260	Human	sec	928	2.7	131	3	AAAG37424	Aag37424	Arabidops
856	2.7	114	4	AAW80066	Human	pro	929	2.7	131	4	AAU48942	Aau48942	Propionib
857	2.7	115	4	AAU21302	Human	nov	930	2.7	131	6	ABW45461	AbW45461	Propionib
858	2.7	116	4	ABG29960	Novel	hum	931	2.7	131	8	ADT55960	AdT55960	Plant pol
859	2.7	116	5	AAE25941	Soybean	G	932	2.7	132	2	AAW55365	Aaw55365	H. pylori
860	2.7	116	6	ABU67338	Soybean	G	933	2.7	132	3	AAAG01051	Aag01051	Human sec
861	2.7	116	8	ADY78257	Plant	ful	934	2.7	132	3	AAAG36582	Aag36582	Arabidops
862	2.7	116	8	ABE11240	Soybean	G	935	2.7	132	4	ABBI1003	AbB11003	Human sec
863	2.7	116	9	AEB48361	Soybean	G	936	2.7	134	5	ABP40764	AbP40764	Staphyloc
864	2.7	117	2	AAW28002	Amino	act	937	2.7	134	5	ABBS7221	AbB57221	Mouse isc
865	2.7	117	4	AAU36840	Staphyloc		938	2.7	134	7	ADBE2496	AdB2496	Human pro
866	2.7	117	4	AAU37274	Staphyloc		939	2.7	134	7	ADBE2494	AdB2494	Rat prote
867	2.7	117	4	AAU37501	Staphyloc		940	2.7	134	7	ABO78213	AbO78213	Pseudom
868	2.7	117	6	AAW72404	Staphyloc		941	2.7	134	8	ADSO8081	AdS08081	Staphyloc
869	2.7	117	7	ADD35694	Human	hep	942	2.7	134	8	ADX68658	AdX68658	Plant ful
870	2.7	118	4	AAW74149	Human	col	943	2.7	134	9	AEB91378	AbE91378	Microbial
871	2.7	119	3	AAI13260	Human	met	944	2.7	135	5	ABR89058	AbR89058	Human pol
872	2.7	119	4	ABBI5306	Human	ner	945	2.7	135	5	ABP32977	AbP32977	Human ORF
873	2.7	119	5	ABP35342	Human	ORF	946	2.7	135	8	ADY06637	AdY06637	Plant ful
874	2.7	119	8	ADT58405	Plant	pol	947	2.7	135	8	ADX95699	AdX95699	Plant ful
875	2.7	120	2	AAW52825	Human	TFE	948	2.7	136	4	AAU43396	Aau43396	Propionib
876	2.7	120	4	AAU61763	Propionib		949	2.7	136	6	ABM13915	AbM13915	Propionib
877	2.7	120	6	ABW58282	Propionib		950	2.7	136	8	ADX94121	AdX94121	Plant ful
878	2.7	120	7	ABW89852	Rice	abio	951	2.7	137	4	AAW85004	Aaw85004	Shrimp wh
879	2.7	121	8	ADW86465	Aspergill		952	2.7	137	5	ADG79542	AdG79542	Human sec
880	2.7	122	4	AAU40049	Propionib		953	2.7	137	8	ADY11590	AdY11590	Plant ful
881	2.7	122	4	AAU64680	Propionib		954	2.7	138	6	ABR43148	AbR43148	Ryegrass
882	2.7	122	4	AAU67329	Propionib		955	2.7	138	7	ABO70911	AbO70911	Pseudom
883	2.7	122	6	ABW63848	Propionib		956	2.7	139	4	ABG09938	AbG09938	Novel hum
884	2.7	122	6	ABW61199	Propionib		957	2.7	139	7	ABO73918	AbO73918	Pseudom
885	2.7	122	6	ABW36568	Propionib		958	2.7	139	8	ADX72208	AdX72208	Plant ful
886	2.7	122	8	ADJ46391	B. subcili		959	2.7	140	3	AAAG4909	AaG4909	Zea maye
887	2.7	122	8	ADW89359	Mouse	ser	960	2.7	140	4	AAW79392	Aaw79392	Human pro
888	2.7	123	3	AAW96514	P. furios		961	2.7	140	7	ADP06215	AdP06215	Bacterial
889	2.7	123	3	ABH11154	Human	sec	962	2.7	140	8	ADX71124	AdX71124	Plant ful
890	2.7	124	3	AAW25953	Zea	maye	963	2.7	141	3	AAAG10064	Aag10064	Arabidops
891	2.7	124	4	AAW88443	Human	Imm	964	2.7	141	3	AAAG37423	Aag37423	Arabidops
892	2.7	124	4	AAO03526	Human	pol	965	2.7	141	6	ADW5626	AdW5626	Human sig
893	2.7	124	5	ABP40499	Staphyloc		966	2.7	141	6	ABU61051	AbU61051	Human ova
894	2.7	124	8	ADSO6053	Staphyloc		967	2.7	141	6	ABU61051	AbU61051	Human ova
895	2.7	124	8	ADW89798	Plant	ful	968	2.7	142	4	ABBB94189	AbB94189	Human nov
896	2.7	125	3	AAW40767	Human	ORF	969	2.7	142	4	ABBB68675	AbB68675	Drosophi
897	2.7	125	4	AAW16497	Peptide	#	970	2.7	142	4	AAW62638	Aaw62638	Novel hum
898	2.7	125	4	ABW35483	Peptide	#	971	2.7	142	4	ABG05888	AbG05888	Novel hum
899	2.7	125	4	AAW28985	Peptide	#	972	2.7	142	5	ABP35032	AbP35032	Human ORF
900	2.7	125	4	ABW30311	Peptide	#	973	2.7	142	6	ABW59157	AbW59157	Propionib

974	6	2.7	142	8	AD142470	Plant tra
975	6	2.7	143	3	AA93242	Antescher
976	6	2.7	143	7	ADH87764	Enterococ
977	6	2.7	143	8	ADO22037	Silicibac
978	6	2.7	143	8	ADY05647	Plant ful
979	6	2.7	143	9	ABE29069	Human OVO
980	6	2.7	143	9	ABE29067	Human OVO
981	6	2.7	144	3	ABE25420	Pinus rad
982	6	2.7	145	3	ABA3074	Human ORF
983	6	2.7	146	4	ABG20929	Novel hum
984	6	2.7	146	5	ADK35186	Novel hum
985	6	2.7	146	6	ABU33774	Protein e
986	6	2.7	147	6	ABP60617	Human hum
987	6	2.7	148	3	AA945233	Arabidops
988	6	2.7	148	7	ABO77145	Pseudomon
989	6	2.7	149	3	AA917619	Arabidops
990	6	2.7	149	4	ABG07326	Novel hum
991	6	2.7	149	4	ABG29930	Novel hum
992	6	2.7	149	7	ADH84387	MSRV-1 as
993	6	2.7	149	7	ADM26145	Hyperther
994	6	2.7	149	8	ADG14833	MSRV asso
995	6	2.7	151	2	AA959910	Opacity a
996	6	2.7	151	3	AA948037	Arabidops
997	6	2.7	151	3	AA918704	Arabidops
998	6	2.7	151	3	AA932302	Arabidops
999	6	2.7	151	8	ADO62119	Tranacrip
1000	6	2.7	152	3	AA956429	Human pro

ALIGNMENTS

RESULT 1
ADPF74494
ID ADF74494 standard; protein; 220 AA.

AC ADF74494;

DT 26-FEB-2004 (first entry)

DE Murine elf-3 protein used to treat end stage liver disease.

XX murine; mouse; early liver development; end stage liver disease; elf 1-3;
 XX mylor-1 (145); pk; protein 106; praja-1; hepatocyte lineage; cholestasis;
 XX biliary stone; hepatic obstruction; stricture; primary biliary cirrhosis;
 XX primary sclerosing cholangitis; gene therapy;
 XX anhidrotic ectoderm dysplasia; hepatocellular carcinoma; anaemia; ataxia;
 XX neurological disorder; haemochromatosis; hepatotropic; cyrostatic;
 XX neuroprotective; antiataemic; cardiant.

OS Mus musculus.

XX US6642362-B1.

PN 04-NOV-2003.

PD 01-NOV-1999; 99US-00431184.

PF 30-APR-1997; 97US-00841349.

PR 30-APR-1998; 98WO-US008656.

XX (MISH/) MISHRA L.

XX Mishra L;

DR WPI, 2003-851362/79.

DR N-PSDB; ADPF74493.

PT New antibodies recognizing early liver development proteins, useful as
 PT markers, in identifying peptides and proteins having early liver
 PT development characteristics, tracing hepatocyte lineage or treating liver
 PT disease.

PS Disclosure; SEQ ID NO 7; 82pp; English.
 XX This invention relates to novel genes and encoded proteins thereof.
 XX isolated during early liver development that are useful in the diagnosis
 CC and treatment of end stage liver disease and other disorders.
 CC Specifically, it refers to genes that encode proteins such as elf 1-3,
 CC mylor-1 (145), pk, protein 106 and praja-1. The present invention
 CC describes the characterisation of these early liver development proteins,
 CC and also methods to raise peptide specific antibodies that are useful as
 CC markers, as well as for tracing hepatocyte lineage. Furthermore, elf
 CC proteins 1-3 are useful in treating disorders including cholestasis,
 CC biliary stones, hepatic obstruction, stricture, primary biliary cirrhosis
 CC or primary sclerosing cholangitis. In addition, through using gene
 CC therapy, praja-1, mylor-1 (145) and pk can be used to treat anhidrotic
 CC ectoderm dysplasia, hepatocellular carcinoma and other diseases including
 CC anaemia, ataxia, degenerative neurological disorders and
 CC haemochromatosis. Accordingly, these proteins can be described as
 CC hepatotropic, cyrostatic, neuroprotective, antiataemic and cardiant. This
 CC polypeptide sequence is the murine elf-3 protein of the invention.

SQ Sequence 220 AA;

Query Match 100.0%; Score 220; DB 7; Length 220;
 Beef Local Similarity 100.0%; Pred. No. 4,7e-208;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEIQRTSSISGPLSPAYTGVPPYNNQLEGRFKQLODEREAVQKTFKWNSHLARVSC	60
DB	1	MELQRTSSISGPLSPAYTGVPPYNNQLEGRFKQLODEREAVQKTFKWNSHLARVSC	60
QY	61	RITDLITDLRDGRMLIKLEVLSEGRLEPKTKGRNRITCLENVKALQFLKEORHLENN	120
DB	61	RITDLITDLRDGRMLIKLEVLSEGRLEPKTKGRNRITCLENVKALQFLKEORHLENN	120
QY	121	GSHDIVDGNHRLITLLELVRRQOEERKORPPSPDPNTKYSEAESEQMDTSKQDVS	180
DB	121	GSHDIVDGNHRLITLLELVRRQOEERKORPPSPDPNTKYSEAESEQMDTSKQDVS	180
QY	181	QNGLPABEQSPRVSYRSQTYQNYKNFNSRRRTASDHSWGM	220
DB	181	QNGLPABEQSPRVSYRSQTYQNYKNFNSRRRTASDHSWGM	220

RESULT 2
ADQ88366
ID ADQ88366 standard; protein; 220 AA.

AC ADQ88366;

DT 07-OCT-2004 (first entry)

DE Mouse elf-3 protein.

XX Early liver developmental protein; liver disease;
 XX hepatocellular carcinoma; anhidrotic ectoderm dysplasia;
 XX degenerative neurological disorder; anaemia; ataxia; haemochromatosis;
 XX sideroblastic anaemia; spinocerebellar ataxia; cholestasis;
 XX biliary stone; liver obstruction; stricture; primary biliary cirrhosis;
 XX primary sclerosing cholangitis; colon cancer; therapy; mouse; elf-1,
 XX embryonic liver; fodrin; beta spectrin.

OS Mus musculus.

XX US2004142354-A1.

PN 22-UTL-2004.

PD 30-OCT-2003; 2003US-00695994.

PF 30-APR-1997; 97US-00841349.

PR 30-APR-1998; 98WO-US008656.
 PR 01-NOV-1999; 99US-00431184.

PA (MISH/) MISHRA L.
 XX
 XX Mishra L;
 PI
 XX WPI, 2004-552558/53.
 DR N-PSDB; ADO88365.
 XX
 PT Novel isolated early liver developmental proteins such as elf, liver-1
 PT (145), pk, protein 106 and praja-1, useful for treating end stage liver
 PT disease, hepatocellular carcinoma, anemia and ataxia.
 XX
 PS Claim 2; SEQ ID NO 7; 85bp; English.
 XX
 CC The invention provides novel early liver developmental proteins such as
 CC elf (embryonic liver fodrin or beta spectrin) 1-3, liver-1 (145), pk,
 CC protein 106 and praja-1 and nucleic acid molecules encoding such
 CC proteins. Other genes coding for early liver developmental proteins
 CC include genes 20, 36, 41, 112, 114, 118 and 129. Polynucleotides of the
 CC invention are useful for treating diseases chosen from end stage liver
 CC disease, hepatocellular carcinoma, anhidrotic ectoderm dysplasia,
 CC degenerative neurological disorders, anaemia, ataxia, haemochromatosis,
 CC sideroblastic anemia and spinocerebellar ataxia. elf sequences are
 CC useful for treating liver disorders chosen from cholestasis, biliary
 CC stones, liver obstruction, stricture, primary biliary cirrhosis and
 CC primary sclerosing cholangitis. praja-1 sequences are useful for
 CC detecting colon cancer. The present sequence is mouse early liver
 CC developmental protein.
 XX
 SQ Sequence 220 AA;

Query Match 100.0%; Score 220; DB 8; Length 220;
 Best Local Similarity 100.0%; Pred. No. 4.7e-208;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELQRTSSISGPLSPAYTGVPYNNQLEGRFKQLQDEREAVOKKTFKWNVSHLARVSC 60
 DB 1 MELQRTSSISGPLSPAYTGVPYNNQLEGRFKQLQDEREAVOKKTFKWNVSHLARVSC 60
 QY 61 RTDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHICLENVDKALQFLKEQRYHLENM 120
 DB 61 RTDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHICLENVDKALQFLKEQRYHLENM 120
 QY 121 GSHDIVDGNHRLTLELEVRQOEERKRRPSPDPNTKVSSEASQOMDTSKGDVVS 180
 DB 121 GSHDIVDGNHRLTLELEVRQOEERKRRPSPDPNTKVSSEASQOMDTSKGDVVS 180
 QY 181 QNGLPABQSGPRVSYRSQTYQNYKNFNSRRTASDHSWSGM 220
 DB 181 QNGLPABQSGPRVSYRSQTYQNYKNFNSRRTASDHSWSGM 220

RESULT 3
 ID AAW81640 standard; protein; 220 AA.
 XX
 AC AAW81640;
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Mouse elf-3 protein.
 XX
 KW Elf-3; mouse; liver development; signal transduction; biliary tree;
 KW cholestasis; biliary stone; hepatic obstruction; stricture;
 KW primary biliary cirrhosis; primary sclerosing cholangitis; therapy.
 XX
 OS Mus sp.
 XX
 PN WO9848827-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 30-APR-1998; 98WO-US008656.
 XX

PR 30-APR-1997; 97US-00841349.
 XX
 XX (MISH/) MISHRA L.
 XX
 XX Mishra L;
 PI
 XX WPI, 1999-009382/01.
 DR N-PSDB; AAV64413.
 XX
 PT New isolated early liver development genes - used to develop products for
 PT treating, e.g. liver disease, hepatocellular carcinoma, degenerative
 PT neurological disorders, anaemia, ataxia or haemochromatosis.
 XX
 PS Claim 9; Fig 2c; 92bp; English.
 XX

CC This is the amino acid sequence of the elf-3 protein of the foetal murine
 CC liver. The invention provides early developing liver proteins (see
 CC AAW81638-42) and the genes coding for them (see AAV64410-24). The genes
 CC were isolated from embryonic cDNA libraries using subtractive
 CC hybridisation. 3 Elf genes (see AAV6441-13) were identified. The elf
 CC proteins (see also AAW81639) are probably important for the formation of
 CC the biliary tree during early liver development. They are used in a
 CC claimed method to treat cholestasis, biliary stones, liver obstruction,
 CC stricture, primary biliary cirrhosis and primary sclerosing cholangitis.
 CC Early developing liver proteins and nucleic acids can also be used in the
 CC diagnosis of liver diseases and other disorders, including those relating
 CC to oncogenesis and tissue repair
 XX
 SQ Sequence 220 AA;

Query Match 58.6%; Score 129; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 2.2e-118;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELQRTSSISGPLSPAYTGVPYNNQLEGRFKQLQDEREAVOKKTFKWNVSHLARVSC 60
 DB 1 MELQRTSSISGPLSPAYTGVPYNNQLEGRFKQLQDEREAVOKKTFKWNVSHLARVSC 60
 QY 61 RTDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHICLENVDKALQFLKEQRYHLENM 120
 DB 61 RTDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHICLENVDKALQFLKEQRYHLENM 120
 QY 121 GSHDIVDGN 129
 DB 121 GSHDIVDGN 129

RESULT 4
 ID ADF13682 standard; protein; 1022 AA.
 XX
 AC ADF13682;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Mouse beta II spectrin amino acid sequence #SEQ ID 2.
 XX
 KW Gene therapy; Sjogren's Syndrome; beta II spectrin.
 XX
 OS Mus sp.
 XX
 PN WO2003100426-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 20-MAY-2003; 2003WO-US016103.
 XX
 PR 20-MAY-2002; 2002US-0381899P.
 XX
 PA (UYWR-) UNIV WRIGHT STATE.
 PA (UYWA) UNIV YALE.
 XX
 PI Brown TL, Morrow JS;

XX WPI, 2004-062080/06.
DR N-PEDB; ADF13681.
PT Identifying primary and secondary Sjogren's Syndrome or susceptibility to
PT developing the disease by contacting the sample with a target antigen and
PT detecting the presence of autoantibodies in the sample that bind to the
PT target antigen.
PS Disclosure; SEQ ID NO 2; 40bp; English.
XX The invention relates to a method for identifying primary and secondary
CC Sjogren's Syndrome, or a susceptibility to developing primary and
CC secondary Sjogren's Syndrome. The method comprises obtaining a biological
CC sample from the subject, contacting the sample with a purified target
CC antigen, where the target antigen is an epitope of beta II spectrin and
CC detecting the presence of autoantibodies in the sample which bind to the
CC target antigen. The method is useful for identifying primary and
CC secondary Sjogren's Syndrome or susceptibility to developing primary and
CC pathological effects of primary and secondary Sjogren's Syndrome. The
CC current sequence represents the mouse beta II spectrin amino acid
CC sequence.
SQ Sequence 1022 AA;

Query Match 56.4%; Score 124; DB 8; Length 1022;
Best Local Similarity 100.0%; Pred. No. 7e-113;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 SGPSPATYGVPPVNNYQLEGRFKQLODEREAVOKKFTKWNVSHLAVSCRTIDLYTDL 69
DB 10 SGPSPATYGVPPVNNYQLEGRFKQLODEREAVOKKFTKWNVSHLAVSCRTIDLYTDL 69
OY 70 RGGRLIKLLEVLSGERLPEKPTKGRMRHICLENVDKALQFLKEQVHLENNGSHDIVDGN 129
DB 70 RGGRLIKLLEVLSGERLPEKPTKGRMRHICLENVDKALQFLKEQVHLENNGSHDIVDGN 129
OY 130 HRLT 133
DB 130 HRLT 133

RESULT 5
AAW81639
ID AAW81639 standard; protein; 2154 AA.

XX AAW81639;
AC AAW81639;
XX 01-MAR-1999 (first entry)
XX Mouse elf-1 protein.
XX elf-1; mouse; liver development; signal transduction; biliary tree;
XX cholestasis; biliary stone; hepatic obstruction; stricture;
XX primary biliary cirrhosis; primary sclerosing cholangitis; therapy.
XX Mus sp.
XX WO9848827-A1.
XX 05-NOV-1998.
XX 30-APR-1998; 98WO-US008656.
XX 30-APR-1997; 97US-00841349.
XX (MISH/) MISHRA L.
XX Mishra L;
XX WPI, 1999-009382/01.
DR N-PEDB; AAV64411.

XX New isolated early liver development genes - used to develop products for
PT treating, e.g. liver disease, hepatocellular carcinoma, degenerative
PT neurological disorders, anaemia, ataxia or haemochromatosis.
PS Claim 9; Fig 2a; 92pp; English.

XX This is the amino acid sequence of the elf-1 protein of the developing
CC murine foetal liver. The invention provides early developing liver
CC proteins (see AAW81638-42) and the genes coding for them (see AAV64410-
CC 24). The genes were isolated from embryonic cDNA libraries using
CC subtractive hybridisation. 3 elf genes (see AAV64411-13) were identified.
CC The elf proteins (see also AAW81640) are probably important for the
CC formation of the biliary tree during early liver development. They are
CC used in a claimed method to treat cholestasis, biliary stones, liver
CC obstruction, stricture, primary biliary cirrhosis and primary sclerosing
CC cholangitis. Early developing liver proteins and nucleic acids can also
CC be used in the diagnosis of liver diseases and other disorders, including
CC those relating to oncogenesis and tissue repair

SQ Sequence 2154 AA;

Query Match 56.4%; Score 124; DB 2; Length 2154;
Best Local Similarity 100.0%; Pred. No. 1.3e-112;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 SGPSPATYGVPPVNNYQLEGRFKQLODEREAVOKKFTKWNVSHLAVSCRTIDLYTDL 69
DB 10 SGPSPATYGVPPVNNYQLEGRFKQLODEREAVOKKFTKWNVSHLAVSCRTIDLYTDL 69
OY 70 RGGRLIKLLEVLSGERLPEKPTKGRMRHICLENVDKALQFLKEQVHLENNGSHDIVDGN 129
DB 70 RGGRLIKLLEVLSGERLPEKPTKGRMRHICLENVDKALQFLKEQVHLENNGSHDIVDGN 129
OY 130 HRLT 133
DB 130 HRLT 133

RESULT 6
ADF74491
ID ADF74491 standard; protein; 2154 AA.

XX ADF74491;
AC ADF74491;
XX 26-FEB-2004 (first entry)
XX Murine elf-1 protein used to treat end stage liver disease.
XX murine; mouse; early liver development; end stage liver disease; elf 1-3;
XX liver-1 (145); pk; protein 106; praja-1; hepatocyte lineage; cholestasis;
XX biliary stone; hepatic obstruction; stricture; primary biliary cirrhosis;
XX primary sclerosing cholangitis; gene therapy;
XX anidrotic ectoderm dysplasia; hepatocellular carcinoma; anaemia; ataxia;
XX neurological disorder; haemochromatosis; hepatotropic; cytostatic;
XX neuroprotective; anti-naemic; cardiant.
XX Mus musculus.
XX US6642362-B1.
XX 04-NOV-2003.
XX 01-NOV-1999; 99US-00431184.
XX 30-APR-1997; 97US-00841349.
XX 30-APR-1998; 98WO-US008656.
XX (MISH/) MISHRA L.
XX Mishra L;
XX WPI, 2003-851362/79.

DR N-PSDB; ADF74490.
XX
PT New antibodies recognizing early liver development proteins, useful as
PT markers, in identifying peptides and proteins having early liver
PT development characteristics, tracing hepatocyte lineage or treating liver
PT disease.
XX
PS Disclosure; SEQ ID NO 4; 82pp; English.
XX
CC This invention relates to novel genes and encoded proteins thereof,
CC isolated during early liver development that are useful in the diagnosis
CC and treatment of end stage liver disease and other disorders.
CC Specifically, it refers to genes that encode proteins such as elf 1-3,
CC 11yor-1 (145), pk, protein 106 and praja-1. The present invention
CC describes the characterization of these early liver development proteins,
CC and also methods to raise peptide specific antibodies that are useful as
CC markers, as well as for tracing hepatocyte lineage. Furthermore, elf
CC proteins 1-3 are useful in treating disorders including cholestasis,
CC biliary stones, hepatic obstruction, stricture, primary biliary cirrhosis
CC or primary sclerosing cholangitis. In addition, through using gene
CC therapy, praja-1, 11yor-1 (145) and pk can be used to treat anhidrotic
CC ectoderm dysplasia, hepatocellular carcinoma and other diseases including
CC anaemia, ataxia, degenerative neurological disorders and
CC haemochromatosis. Accordingly, these proteins can be described as
CC hepatotropic, cytosstatic, neuroprotective, antanaemic and cardiant. This
CC polypeptide sequence is the murine elf-1 protein of the invention.
XX
SQ Sequence 2154 AA;

Query Match 56.4%; Score 124; DB 7; Length 2154;
Best Local Similarity 100.0%; Pred. No. 1.3e-112;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SGPSPATGVPPVNNOLBGRFQLODERAVQKTTTKVNSHLAVSCRITDLYTDL 69
DB 10 SGPSPATGVPPVNNOLBGRFQLODERAVQKTTTKVNSHLAVSCRITDLYTDL 69
DB 70 RDGRMLIKLLEVLSEGERLPKPTKGRMRHICLENVDKALQFLKEORVHLENNGSHDIVDGN 129
QY 130 HRLT 133
DB 130 HRLT 133
DB 130 HRLT 133

RESULT 7
ADQ88363
ID ADQ88363 standard; protein; 2154 AA.
XX
AC ADQ88363;
XX
DT 07-OCT-2004 (first entry)
XX
DE Mouse elf-1 protein.
XX
KM Early liver developmental protein; liver disease;
KM hepatocellular carcinoma; anhidrotic ectoderm dysplasia;
KM degenerative neurological disorder; anaemia; ataxia; haemochromatosis;
KM sideroblastic anaemia; spinocerebellar ataxia; cholestasis;
KM biliary stone; liver obstruction; stricture; primary biliary cirrhosis;
KM primary sclerosing cholangitis; colon cancer; therapy; mouse; elf-1;
KM embryonic liver fodrin; beta spectrin.
XX
OS Mus musculus.
XX
PN US2004142354-A1.
XX
PD 22-JUL-2004.
XX
PF 30-OCT-2003; 2003US-00695994.
XX
PR 30-APR-1997; 97US-00841349.

PR 30-APR-1998; 98WO-US008656.
PR 01-NOV-1999; 99US-00431184.
XX
PA (MISH/) MISHRA L.
XX
PI Mishra L;
XX
DR WPI; 2004-552558/53.
DR N-PSDB; ADQ88362.
XX
PT Novel isolated early liver developmental proteins such as elf, 11yor-1
PT (145), pk, protein 106 and praja-1, useful for treating end stage liver
PT disease, hepatocellular carcinoma, anemia and ataxia.
XX
PS Disclosure; SEQ ID NO 4; 85pp; English.
XX
CC The invention provides novel early liver developmental proteins such as
CC elf (embryonic liver fodrin or beta spectrin) 1-3, 11yor-1 (145), pk,
CC protein 106 and praja-1 and nucleic acid molecules encoding such
CC proteins. Other genes coding for early liver developmental proteins
CC include genes 20, 36, 41, 112, 114, 118 and 129. Polynucleotides of the
CC invention are useful for treating diseases chosen from end stage liver
CC disease, hepatocellular carcinoma, anhidrotic ectoderm dysplasia,
CC degenerative neurological disorders, anaemia, ataxia, haemochromatosis,
CC sideroblastic anaemia and spinocerebellar ataxia. elf sequences are
CC useful for treating liver disorders chosen from cholestasis, biliary
CC stones, liver obstruction, stricture, primary biliary cirrhosis and
CC primary sclerosing cholangitis. praja-1 sequences are useful for
CC detecting colon cancer. The present sequence is mouse early liver
CC developmental protein.
XX
SQ Sequence 2154 AA;

Query Match 56.4%; Score 124; DB 8; Length 2154;
Best Local Similarity 100.0%; Pred. No. 1.3e-112;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SGPSPATGVPPVNNOLBGRFQLODERAVQKTTTKVNSHLAVSCRITDLYTDL 69
DB 10 SGPSPATGVPPVNNOLBGRFQLODERAVQKTTTKVNSHLAVSCRITDLYTDL 69
DB 70 RDGRMLIKLLEVLSEGERLPKPTKGRMRHICLENVDKALQFLKEORVHLENNGSHDIVDGN 129
QY 130 HRLT 133
DB 130 HRLT 133
DB 130 HRLT 133

RESULT 8
ADZ85101
ID ADZ85101 standard; protein; 2154 AA.
XX
AC ADZ85101;
XX
DT 14-JUL-2005 (first entry)
XX
DE Full-length FHOS interacting protein, SEQ ID 150.
XX
KM FHOS; antiinflammatory; neuroprotective; cytosstatic; cardiovascular-Gen.;
KM antidiabetic; inflammation; neurodegenerative disease; cancer;
KM cardiovascular disease; diabetes mellitus.
XX
OS Mus musculus.
XX
PN US2005100966-A1.
XX
PD 12-MAY-2005.
XX
PF 19-MAR-2004; 2004US-00805684.
XX
PR 02-APR-2003; 2003US-045936P.

PR 02-APR-2003; 2003US-0460103P.
 PR 03-JUN-2003; 2003US-0455766P.
 XX
 XX (SAKA/) SAKAMOTO T.
 PA (TAKE/) TAKEDA S.
 XX
 PI Sakamoto T, Takeda S;
 XX WPI, 2005-345401/35.
 DR
 XX Novel isolated protein comprising FHOS or its homolog, derivative or
 PT fragment, interacting with protein chosen from group of GROUP1 e.g.
 PT MRNP23, MRNP59 or MRBD7(627), useful for screening its modulator.
 XX
 PS Disclosure; SEQ ID NO 150; 163pp; English.
 XX
 XX The invention relates to a novel isolated protein comprising a first
 CC protein, which is FHOS or its homolog, derivative or fragment,
 CC interacting with a second protein chosen from a group of GROUP1, e.g.
 CC MRNP23, MRNP59 or MRBD7(627), where the interaction is through a complex
 CC or covalent bond, or any other intermolecular interaction. The invention
 CC further comprises: a method for producing the FHOS-interacting protein; a
 CC method for detecting the FHOS-interacting protein in a sample; a method
 CC for determining whether a compound is capable of modulating an
 CC interaction between a first polypeptide (FHOS) or its homolog, derivative
 CC of fragments) and a second polypeptide as mentioned in the FHOS-
 CC interacting protein; and a method for modulating the function or activity
 CC of the FHOS-interacting protein in cells of a specific tissue of a
 CC mammal. The FHOS-interacting protein has the activities:
 CC antiinflammatory, neuroprotective, cytoskeletal, cardiovascular-Gen., and
 CC antidiabetic. The FHOS-interacting protein is useful for selecting its
 CC modulators. The method for modulating the function or activity of the
 CC FHOS-interacting protein in cells of a specific tissue is useful for
 CC treating inflammatory diseases, neurodegenerative diseases, cancer,
 CC cardiovascular diseases or diabetes mellitus. This sequence represents an
 CC FHOS interacting protein for use in the novel protein complex of the
 CC invention.
 CC
 XX Sequence 2154 AA:
 SQ
 Query Match 56.4%; Score 124; DB 9; Length 2154;
 Best Local Similarity 100.0%; Pred. No. 1.3e-112;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 SGPISPAAYTGVYNNNOLEGRFKQIDREAVOKKFTKWNVSHLARSCTITDLYTL 69
 DB 10 SGPISPAAYTGVYNNNOLEGRFKQIDREAVOKKFTKWNVSHLARSCTITDLYTL 69
 QY 70 RDGRMLIKLEVLSEGRLEPKPTKGRMRHICLENVDKALQFLKEQRVHLENMGSMDIVDGN 129
 DB 70 RDGRMLIKLEVLSEGRLEPKPTKGRMRHICLENVDKALQFLKEQRVHLENMGSMDIVDGN 129
 QY 130 HRLT 133
 DB 130 HRLT 133
 RESULT 9
 ABUT0467
 ID ABUT0467 standard; protein; 321 AA.
 XX
 AC ABUT0467;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Human adipocyte Selected Interacting domain, SID, #98.
 XX
 KM Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KM antidiabetic; protein-protein interaction; diabetes;
 XX yeast 2-hybrid assay; metabolic disorder; obesity.
 XX
 KM Homo sapiens.
 OS
 XX

PN W0200286122-A2.
 XX
 XX 31-OCT-2002.
 PD
 XX
 XX 14-MAR-2002; 2002MO-EP003768.
 PF
 XX
 PR 14-MAR-2001; 2001US-0275734P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P, Davlet L;
 XX WPI, 2003-103412/09.
 DR N-PSDB; ACA57011.
 DR
 XX
 PT New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 XX obesity or diabetes.
 PS
 XX Claim 6; Page 144; 382pp; English.
 CC
 CC The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a
 CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention
 CC
 XX Sequence 321 AA:
 SQ
 Query Match 44.1%; Score 97; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 DEREAVOKKFTKWNVSHLARSCTITDLYTLRDGRMLIKLEVLSEGRLEPKPTKGRMR 96
 DB 23 DEREAVOKKFTKWNVSHLARSCTITDLYTLRDGRMLIKLEVLSEGRLEPKPTKGRMR 82
 QY 97 IHLENVDKALQFLKEQRVHLENMGSMDIVDGNHRLT 133
 DB 83 IHLENVDKALQFLKEQRVHLENMGSMDIVDGNHRLT 119
 RESULT 10
 ABUT0517
 ID ABUT0517 standard; protein; 341 AA.
 XX
 AC ABUT0517;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Human adipocyte Selected Interacting domain, SID, #148.
 XX
 KM Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KM antidiabetic; protein-protein interaction; diabetes;
 XX

KW Yeast 2-hybrid assay; metabolic disorder; obesity.
XX
OS Homo sapiens.
XX
FN WO200286122-A2.
XX
PD 31-OCT-2002.
XX
PF 14-MAR-2002; 2002MO-EP003766.
XX
PR 14-MAR-2001; 2001US-0275734P.
XX
PA (HYBR-) HYBRIGENICS.
XX
PI Legrain P, Daviet L;
XX
DR WPI; 2003-103412/09.
XX
N-PSDB; ACAS7061.
XX
PT New complex between two interacting proteins in adipocyte cells, useful
PT for identifying selected interacting domains that modulate protein
PT interactions, or for preventing or treating metabolic disorders such as
PT obesity or diabetes.
XX
PS Claim 6; Page 156-157; 382pp; English.
XX
CC The invention relates to a complex between two interacting proteins in
CC adipocyte cells, given in the specification. The proteins are identified
CC by selecting a bait protein from a known adipocyte marker and then
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
CC members of an adipocyte cDNA library. The proteins are designated SID
CC (RTM) (selected interacting domains) proteins. Also included are a
CC polynucleotide encoding a polypeptide in the adipocyte cells, a
CC recombinant host cell expressing at least one of the interacting
CC polypeptides of the complex, selecting a modulating compound in adipocyte
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
CC sequences given in the specification (including its fragment or variant),
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
CC given in the specification (including its fragment or variant), a vector
CC comprising the SID (RTM) polynucleotide, a recombinant host cell
CC comprising the vector, a protein chip comprising the polypeptides and a
CC record comprising all or part of the data, listed in the specification.
CC The complex, polypeptides, polynucleotides and compounds are useful for
CC preventing or treating metabolic disorders such as obesity or diabetes.
CC The polynucleotides are useful as probes or primers. The complex is
CC particularly useful for identifying selected interacting domains (SID
CC (RTM)) for screening drugs that modulate the protein interaction, thus
CC exhibiting the therapeutic effect. The present sequence represents a SID
CC (prey) protein of the invention
XX
SQ Sequence 341 AA;
XX
Query Match 44.1%; Score 97; DB 6; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 DEREAIVQKTKFTKWNVSHLARVSCRTIDLYDLRGRMLIKLEVLSEGRLPKPTKGRMR 96
DB 39 DEREAIVQKTKFTKWNVSHLARVSCRTIDLYDLRGRMLIKLEVLSEGRLPKPTKGRMR 98
QY 97 IHCLENVDKALQFLKEQRVHLENNGSHDIYDGNHRLT 133
DB 99 IHCLENVDKALQFLKEQRVHLENNGSHDIYDGNHRLT 135
XX
RESULT 11
ID ADJ70625 standard; protein; 1630 AA.
XX
AC ADJ70625;
XX
DT 06-MAY-2004 (first entry)
XX

DE Human heat mitochondrial protein as a therapeutic target SegID2431.
XX
KW Mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cyostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
XX
PR 17-JUN-2002; 2002US-0389987P.
XX
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
XX
PA (BUCK-) BUCK INSTR AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2431; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 1630 AA;
XX
Query Match 44.1%; Score 97; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 4.7e-86;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 DEREAIVQKTKFTKWNVSHLARVSCRTIDLYDLRGRMLIKLEVLSEGRLPKPTKGRMR 96
DB 50 DEREAIVQKTKFTKWNVSHLARVSCRTIDLYDLRGRMLIKLEVLSEGRLPKPTKGRMR 109
QY 97 IHCLENVDKALQFLKEQRVHLENNGSHDIYDGNHRLT 133
DB 110 IHCLENVDKALQFLKEQRVHLENNGSHDIYDGNHRLT 146
XX
RESULT 12
ID ABP65068 standard; protein; 2364 AA.
XX
AC ABP65068;
XX

XX 12-NOV-2002 (first entry)
 XX Hypoxia-induced protein #8.
 DE
 XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
 KM antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
 KM hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
 KM ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
 KM preclapemia; atherosclerosis; inflammatory condition; wound healing;
 KM inflammation; erythropoiesis; hair loss; human.
 XX Homo sapiens.
 OS
 XX WO200246465-A2.
 XX
 XX 13-UN-2002.
 PD
 XX 10-DEC-2001; 2001WO-GB005458.
 XX
 XX 08-DEC-2000; 2000GB-00030076.
 PR 08-FEB-2001; 2001GB-00003156.
 PR 25-OCT-2001; 2001GB-00025666.
 XX
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA
 PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
 PI Rayner WN;
 XX WPI, 2002-627238/67.
 DR
 XX Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.
 XX
 PS Claim 13; Page 271-272; 538pp; English.
 XX
 XX The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV7873-ABV78116
 CC and ABP5061-ABP5257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, preclapemia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss
 CC
 XX
 XX Sequence 2364 AA;
 SQ
 Query Match 44.1%; Score 97; DB 5; Length 2364;
 Best Local Similarity 100.0%; Pred. No. 5.8e-86;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY
 37 DERBAVOKKFTKWNVSHLARVSCRTDLYTLDRGRMLIKLEVLGSRLEPPTKGRMR 96
 DB 50 DERBAVOKKFTKWNVSHLARVSCRTDLYTLDRGRMLIKLEVLGSRLEPPTKGRMR 109
 QY 97 IHCLENVDKALQFLKEQRVHLENGSHDIVDGNHRLT 133
 DB 110 IHCLENVDKALQFLKEQRVHLENGSHDIVDGNHRLT 146
 RESULT 13
 ABM80299

ID ABM80299 standard; protein; 2364 AA.
 XX
 AC ABM80299;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 XX Tumour-associated antigenic target (TAT) polypeptide PRO58543, SEQ.747.
 DE
 XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukaemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytosstatic.
 XX
 OS
 XX Homo sapiens.
 XX
 XX WO2004030615-A2.
 XX
 XX 15-APR-2004.
 PD
 XX 29-SEP-2003; 2003WO-US028547.
 XX
 XX 02-OCT-2002; 2002US-0414971P.
 PR
 XX (GETH) GENENTECH INC.
 XX
 XX Wu TD, Zhang Z, Zhou Y;
 XX
 XX WPI, 2004-347921/32.
 DR N-PSDB; ACN37691.
 XX
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 747; 7273pp; English.
 XX
 XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 CC
 XX
 XX Sequence 2364 AA;
 SQ
 Query Match 44.1%; Score 97; DB 8; Length 2364;
 Best Local Similarity 100.0%; Pred. No. 5.8e-86;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY
 37 DERBAVOKKFTKWNVSHLARVSCRTDLYTLDRGRMLIKLEVLGSRLEPPTKGRMR 96
 DB 50 DERBAVOKKFTKWNVSHLARVSCRTDLYTLDRGRMLIKLEVLGSRLEPPTKGRMR 109
 QY 97 IHCLENVDKALQFLKEQRVHLENGSHDIVDGNHRLT 133
 DB 110 IHCLENVDKALQFLKEQRVHLENGSHDIVDGNHRLT 146
 RESULT 13
 ABM80299

Db 110 IHCLENVDKALQFLKEGRVHLENNGSHDIVDGNHRLT 146

RESULT 14

ADZ70337 ID ADZ70337 standard; protein; 2364 AA.

XX AC ADZ70337;

XX DT 30-JUN-2005 (first entry)

XX DE Human protein from lung cancer marker gene SPTBN1.

XX DE Tumor marker; lung tumor; cytostatic; neoplasm; expression;

XX KM DNA microarray.

XX OS Homo sapiens.

XX PN WO2005032495-A2.

XX PD 14-APR-2005.

XX PF 01-OCT-2004; 2004WO-US034163.

XX PR 03-OCT-2003; 2003US-0508355P.

XX PA (FARB) BAYER PHARM CORP.

XX PI Taylor I, Pauloski NR, Bigwood D,

XX DR WPI; 2005-285325/29.

XX DR N-PSDB; ADZ70336.

XX PT Providing a patient diagnosis for lung cancer comprises comparing the

XX PT level of expression of genes or gene products in a biological sample from

XX PT the patient with that from a normal individual.

XX PS Claim 3; SEQ ID NO 22; 60pp; English.

XX CC The invention relates to providing a patient diagnosis for lung cancer

XX CC comprising comparing the level of expression of genes or gene products in

XX CC a biological sample from the patient with the level of expression of

XX CC genes or gene products in a biological sample from a normal individual.

XX CC Also included are distinguishing between normal and disease tissues,

XX CC monitoring the response of a patient being treated for lung cancer by

XX CC administering an anti-cancer agent, identifying a compound useful for the

XX CC treatment of lung cancer and an array for distinguishing between normal

XX CC and disease tissues (comprising 2 or more probes corresponding to 2 or

XX CC more genes selected from any of the 200 nucleotide sequences given in the

XX CC specification, or 2 or more polypeptides comprising any of the 200 amino

XX CC acid sequences given in the specification). In providing a patient

XX CC diagnosis for lung cancer, one or more genes are selected from any of the

XX CC 200 nucleotide sequences as mentioned in the specification, or one or

XX CC more gene products are polypeptides selected from any of the 20 amino

XX CC acid sequences mentioned in the specification. The methods are useful for

XX CC detecting and treating lung cancer. These may also be used for designing,

XX CC identifying and optimizing therapeutics for cancer. The present sequence

XX CC represents a protein from one of the 200 lung cancer marker genes. Note:

XX CC The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 2364 AA;

Query Match 44.1%; Score 97; DB 9; Length 2364;

Best Local Similarity 100.0%; Pred. No. 5.8e-86;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 DERAVVQKTKTKVNSHLAVSCRTITLYTDIDGRLITLLEVLSESRPKPKTKGMR 96

DB 50 DERAVVQKTKTKVNSHLAVSCRTITLYTDIDGRLITLLEVLSESRPKPKTKGMR 109

OY 97 IHCLENVDKALQFLKEGRVHLENNGSHDIVDGNHRLT 133

Db 110 IHCLENVDKALQFLKEGRVHLENNGSHDIVDGNHRLT 146

RESULT 15

AAW81642 ID AAW81642 standard; protein; 1120 AA.

XX AC AAW81642;

XX DT 01-MAR-1999 (first entry)

XX DE Mouse elf protein.

XX DE Elf; mouse; liver development; signal transduction; biliary tree;

XX KM cholestasis; biliary stone; hepatic obstruction; stricture;

XX KM primary biliary cirrhosis; primary sclerosing cholangitis; therapy.

XX OS Mus sp.

XX PN M09848827-A1.

XX PD 05-NOV-1998.

XX PF 30-APR-1998; 98WO-US008656.

XX PR 30-APR-1997; 97US-00841349.

XX PA (MISH/) MISHRA L.

XX PI Mishra L;

XX DR WPI; 1999-009382/01.

XX DR N-PSDB; AAW84424.

XX PT New isolated early liver development genes - used to develop products for

XX PT treating, e.g. liver disease, hepatocellular carcinoma, degenerative

XX PT neurological disorders, anaemia, ataxia or haemochromatosis.

XX PS Example 2; Fig 16a; 92pp; English.

XX CC This is the amino acid sequence of an elf protein of the foetal murine

XX CC liver, as deduced from an isolated partial cDNA clone (see AAW84424). The

XX CC invention provides early developing liver proteins (see AAW81638-42) and

XX CC the genes coding for them (see AAW84410-24). The genes were isolated from

XX CC embryonic cDNA libraries using subtractive hybridisation. 3 Elf genes

XX CC (see AAW84411-13) were identified. The elf proteins (see also AAW81639-40)

XX CC are probably important for the formation of the biliary tree during

XX CC early liver development. They are used in a claimed method to treat

XX CC cholestasis, biliary stones, liver obstruction, stricture, primary

XX CC biliary cirrhosis and primary sclerosing cholangitis. Early developing

XX CC liver proteins and nucleic acids can also be used in the diagnosis of

XX CC liver diseases and other disorders, including those relating to

XX CC oncogenesis and tissue repair

XX SQ Sequence 1120 AA;

Query Match 40.9%; Score 90; DB 2; Length 1120;

Best Local Similarity 100.0%; Pred. No. 2.4e-79;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 RLTTLLELVRROOEERERGRPPSPPNKVSSEASQOMDSKGNQVONGIPAAQGS 190

DB 1031 RLTTLLELVRROOEERERGRPPSPPNKVSSEASQOMDSKGNQVONGIPAAQGS 1090

OY 191 PRVSYRSQTYQNYKNFNSRRRTASDHSWGM 220

DB 1091 PRVSYRSQTYQNYKNFNSRRRTASDHSWGM 1120

RESULT 16

ADJ70287 ID ADJ70287 standard; protein; 2106 AA.

XX ADJ70287;
 AC 06-MAY-2004 (first entry)
 XX
 DT
 XX
 XX
 DE Human heat mitochondrial protein as a therapeutic target SegID2093.
 XX
 XX
 KW mitochondria; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cyostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 XX 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-038987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 PI Gosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 PI WPI; 2003-845369/78.
 DR
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1: SEQ ID NO 2093; 180pp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondria proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cyostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 2106 AA;
 XX
 Query Match 17.3%; Score 38; DB 7; Length 2106;
 Best Local Similarity 100.0%; Pred. No. 7.4e-28;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 95 MRHICLENVDKALQFLKEORVHLNMGSHDIVDGNHRL 132
 DB 108 MRHICLENVDKALQFLKEORVHLNMGSHDIVDGNHRL 145
 XX
 RESULT 17
 ADX06608 standard; protein; 2137 AA.
 XX

AC ADX06608;
 XX 21-APR-2005 (first entry)
 XX
 DT
 XX
 XX
 DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1173.
 XX
 XX
 KW cyostatic; cyclin-dependent kinase; cdk; biomarker.
 XX
 OS Homo sapiens.
 XX
 PN WO2005012875-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 29-JUL-2004; 2004WO-US024424.
 XX
 PR 29-JUL-2003; 2003US-0490890P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 PI WPI; 2005-163068/17.
 DR P-PSDB; ADX06607.
 XX
 PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX
 PS Claim 5; SEQ ID NO 1173; 141pp; English.
 XX
 CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO.1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-
 CC oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
 CC sequence represents a biomarker used in the method of the invention.
 XX
 SQ Sequence 2137 AA;
 XX
 Query Match 17.3%; Score 38; DB 9; Length 2137;
 Best Local Similarity 100.0%; Pred. No. 7.4e-28;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 95 MRHICLENVDKALQFLKEORVHLNMGSHDIVDGNHRL 132
 DB 108 MRHICLENVDKALQFLKEORVHLNMGSHDIVDGNHRL 145
 XX
 RESULT 18
 ABR41636
 ID ABR41636 standard; protein; 2141 AA.
 XX
 AC ABR41636;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human DITRP cytoskeletal protein.
 XX
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;

KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;
 KW cytoskeletal protein.
 KW
 OS Homo sapiens.
 PN WO200297031-A2.
 PD 05-DEC-2002.
 XX
 XX
 PF 27-MAR-2002; 2002WO-US010056.
 XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291843P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PI Daflo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daugherty SC, Dem TC, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 DR WPI; 2003-129518/12.
 DR N-PSDB; ACC46573.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for identifying
 PT test compound which specifically binds to a polypeptide encoded by human
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
 XX
 .Claim 27; SEQ ID NO 1171; 591pp; English.
 XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated ditrp (ACC46080-ACC46749) and to their encoded
 CC proteins (DITRP; ABR41136-ABR41812). The invention also relates to
 CC polynucleotide sequences at least 90% identical to the ditrp CDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a ditrp nucleic acid sequence; the
 CC recombinant production of DITRP proteins; antibodies specific for DITRP
 CC proteins; microarrays comprising ditrp nucleic acid sequences; methods of
 CC detecting ditrp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITRP protein; and methods of
 CC assessing the toxicity of test compounds using a ditrp hybridisation
 CC probe. Ditrp nucleic acid sequences and DITRP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITRP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The ditrp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITRP protein which is a cytoskeletal
 CC protein. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

SQL Sequence 2141 AA;
 - Query Match 17.3%; Score 38; DB 6; Length 2141;
 - Best Local Similarity 100.0%; Pred. NO. 7.5e-28;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 95 MRHCLENVKALQFLKEQRYHLEMGSHDIVDGNHRL 132
 DB 112 MRHCLENVKALQFLKEQRYHLEMGSHDIVDGNHRL 149.
 RESULT 19
 AAU01183
 ID AAU01183 standard; protein; 2387 AA.
 XX
 XX AAU01183;
 AC
 DT 07-SEP-2001 (first entry)
 XX
 DE Rat glutamate transporter associated protein GTRAP4-41.
 XX
 KW Rat; glutamate transporter associated protein; GTRAP4-41;
 KW glutamate transporter protein; chloride transporter; neurodegeneration;
 KW cytoskeletal stability; nervous system disorder; schizophrenia;
 KW spinocerebellar ataxia type 1; SCAL; GABA metabolism.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2048..2049
 FT /note="Encoded by GTAGGAGC"
 XX
 EN WO200130968-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 23-OCT-2000; 2000WO-US029431.
 XX
 PR 23-OCT-1999; 99US-0161007P.
 PR 22-MAY-2000; 2000US-0206157P.
 XX
 PA (UWJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Rohtstein JD, Jackson M, Lin G, Law R, Orlov I;
 DR WPI; 2001-300498/31.
 DR N-PSDB; AAS04273.
 XX
 PT Novel substantially pure glutamate transporter associated polypeptide
 PT which modulates intracellular glutamate transport, interacts with
 PT glutamate transporter protein and has expression pattern in brain.
 XX
 .Claim 7; Fig 15; 116pp; English.
 XX
 CC The present sequence representing novel rat glutamate transporter
 CC associated protein GTRAP4-41 modulates intracellular glutamate transport,
 CC interacts with a glutamate transporter protein and has an expression
 CC pattern in the brain. The GTRAP proteins are also involved in mediating
 CC chloride transport and cytoskeletal stability. The invention also
 CC provides methods for identifying a compound that modulates a cellular
 CC response mediated by a GTRAP protein and a compound that inhibits the
 CC interaction of a glutamate transporter protein and a GTRAP protein. A
 CC compound which modulates the activity of a glutamate transporter
 CC associated polypeptide or interaction with a glutamate transporter
 CC protein is useful for treating a disorder associated with glutamate
 CC transport or chloride flux, preferably a nervous system disorder such as
 CC neurodegeneration, spinocerebellar ataxia type 1 (SCAL), schizophrenia,
 CC epilepsy or a disorder of GABA metabolism. Such compound could be an
 CC antisense oligonucleotide (AAS04278) which can be used for modulating
 CC glutamate transport in a subject
 XX
 SQ Sequence 2387 AA;

Query Match 12.3%; Score 27; DB 4; Length 2387;
Best Local Similarity 100.0%; Pred. No. 5.7e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LPKPTKGRMRHCHLENDKALQFLKEQ 113
DB 103 LPKPTKGRMRHCHLENDKALQFLKEQ 129

RESULT 20

AA05494
ID AA05494 standard; protein; 2390 AA.

AC AAY05494;

DT 08-JUL-1999 (first entry)

DE BetaIII spectrin protein sequence.

KM BetaIII spectrin; intracellular sequestration modulation; SNAIS;

KM spectrin-ankyrin-adaptor protein trafficking/trafficking system;

KM integral membrane protein; secretory protein; endoplasmic reticulum;

KM cis-Golgi apparatus; medial-Golgi apparatus; trans-Golgi apparatus;

KM plasma cell membrane; cystic fibrosis.

OS Mammalia.

PN WO9916875-A1.

PD 08-APR-1999.

PF 30-SEP-1998; 98WO-US020364.

PR 30-SEP-1997; 97US-0060559P.

PA (UYUA) UNIV YALE.

PI Morrow JS, Devareajan P;

DR WPI; 1999-277085/23.

DR N-PSDB; AAX36583.

PT Modulating intracellular sequestration of a selected integral membrane or

PT secretory protein into a transport vehicle.

PS Claim 21; Fig 19e; 129pp; English.

XX This sequence represents a mammalian betaIII spectrin. The invention
XX relates to a method for modulating intracellular sequestration of a
XX selected integral membrane or secretory protein into a transport vehicle
XX (for transport from the endoplasmic reticulum to the cis-Golgi apparatus,
XX or from the cis-Golgi to the medial-Golgi apparatus, or from the medial-
XX Golgi to the trans-Golgi apparatus or from the trans-Golgi apparatus to
XX the plasma cell membrane) using the spectrin-ankyrin-adaptor protein
XX trafficking/trafficking system (SNAIS). Compounds that inhibit or enhance
XX intracellular sequestration of selected integral membrane or secretory
XX protein into a transport vehicle are useful for ameliorating effects of
XX disease caused by a relative excess or deficit in the amount of the
XX particular protein. Identification of e.g. the binding domain for CPTF
XX (cystic fibrosis transmembrane conductance regulator) responsible for
XX cystic fibrosis, in the spectrin-ankyrin-adaptor protein
XX trafficking/trafficking system (SNAIS), by the methods would allow early
XX analysis of possible transport enhancing reagents that might the clinical
XX synthesis of this disease. The method does not attempt to suppress the
XX synthesis of a given protein, only its delivery to the correct cellular
XX tissue compartment. Intracellular expression of RNA is not required and
XX the method lends itself to high-throughput in vitro screening assays

XX Sequence 2390 AA;

Query Match 12.3%; Score 27; DB 2; Length 2390;

Best Local Similarity 100.0%; Pred. No. 5.7e-17;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LPKPTKGRMRHCHLENDKALQFLKEQ 113
DB 103 LPKPTKGRMRHCHLENDKALQFLKEQ 129

RESULT 21

ABP41709
ID ABP41709 standard; protein; 806 AA.

AC ABP41709;

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HBODF41, SEQ ID NO:2841.

KM Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

KM ovarian cancer; breast cancer; tumour; reproductive system disorder;

KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;

KM inflammatory condition; immune disorder; blood disorder;

KM cardiovascular disorder; respiratory disorder; neurological disorder;

KM gastrointestinal disorder; urinary system disorder; drug screening;

KM gene therapy; chromosome mapping; forensic analysis;

KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;

KM antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

PN WO200200677-A1.

PD 03-JAN-2002.

PF 07-JUN-2001; 2001WO-US018569.

PR 07-JUN-2000; 2000US-0209467P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Birse CE, Rosen CA;

DR WPI; 2002-147878/19.

DR N-PSDB; ABQ54786.

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,

PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian

PT cancer), immune disorders, cardiovascular disorders and neurological

PT diseases.

PS Claim 11; SEQ ID NO 2841; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosis or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 806 AA;

Query Match 10.5%; Score 23; DB 5; Length 806;
 Best Local Similarity 100.0%; Pred. No. 2e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 131 RLTTLELVRRQSEERKRP 153
 Db 699 RLTTLELVRRQSEERKRP 721

RESULT 22

ABB61876
 ID ABB61876 standard; protein; 2291 AA.

XX ABB61876;

AC 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 12420.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL05979.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions.

XX Disclosure; SEQ ID NO 12420; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABL6176-ABL30511), expressed DNA

XX sequences (ABL01840-ABL6175) and the encoded proteins (ABBS7737-

XX ABB12072). The sequence data for this patent did not form part of the

XX printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2291 AA;

XX Query Match 8.6%; Score 19; DB 4; Length 2291;

XX Best Local Similarity 100.0%; Pred. No. 4.2e-09;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 75 LKLEVLGSGRLPKPTKG 93
 Db 84 LKLEVLGSGRLPKPTKG 102

RESULT 23
 ID ADF74518
 ADF74518 standard; peptide; 15 AA.

XX ADF74518;

AC 26-FEB-2004 (first entry)

DT Peptide from the C-terminus of the murine elf 3 protein.

XX murine; mouse; early liver development; end stage liver disease; elf 1-3;

XX 11yor-1 (145); pk; protein 106; praja-1; hepatocyte lineage; cholestasis;

XX biliary stone; hepatic obstruction; stricture; primary biliary cirrhosis;

XX primary sclerosing cholangitis; gene therapy;

XX anhidrotic ectoderm dysplasia; hepatocellular carcinoma; anemia; ataxia;

XX neurological disorder; haemochromatosis; hepatotropic; cytostatic;

XX neuroprotective; antihaemic; cardiac; antibody.

XX Mus musculus.

XX US6642362-B1.

XX 04-NOV-2003.

XX 01-NOV-1999; 99US-00431184.

XX 30-APR-1997; 97US-00841349.

XX 30-APR-1998; 98WO-US008656.

XX (MISH/) MISHRA L.

XX Mishra L;

XX WPI; 2003-851362/79.

XX This invention relates to novel genes and encoded proteins thereof.

XX isolated during early liver development that are useful in the diagnosis

XX and treatment of end stage liver disease and other disorders.

XX Specifically, it refers to genes that encode proteins such as elf 1-3,

XX 11yor-1 (145), pk, protein 106 and praja-1. The present invention

XX describes the characterisation of these early liver development proteins,

XX and also methods to raise peptide specific antibodies that are useful as

XX markers, as well as for tracing hepatocyte lineage. Furthermore, elf

XX proteins 1-3 are useful in treating disorders including cholestasis,

XX biliary stones, hepatic obstruction, stricture, primary biliary cirrhosis

XX or primary sclerosing cholangitis. In addition, through using gene

XX therapy, praja-1, 11yor-1 (145) and pk can be used to treat anhidrotic

XX ectoderm dysplasia, hepatocellular carcinoma and other diseases including

XX anemia, ataxia, degenerative neurological disorders and

XX haemochromatosis. Accordingly, these proteins can be described as

XX hepatotropic, cytostatic, neuroprotective, antihaemic and cardiac. This

XX sequence differs from the C-terminus of the murine elf 3 protein, used

XX sequence listing (SeqID 20).

XX Sequence 15 AA;

XX Query Match 6.8%; Score 15; DB 7; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 4.9e-07;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 FNSRRTASDHWSGSM 220
 DB 1 FNSRRTASDHWSGSM 15

RESULT 24

ADQ88396
 ID ADQ88396 standard; peptide; 15 AA.

AC ADQ88396;

DT 07-OCT-2004 (first entry)

DE Mouse elf-3 epitope peptide #2.

XX Early liver developmental protein; liver disease;
 KW hepatocellular carcinoma; anhidrotic ectoderm dysplasia;
 KW degenerative neurological disorder; anaemia; ataxia; haemochromatosis;
 KW sideroblastic anaemia; spinocerebellar ataxia; Cholestasis;
 KW biliary stone; liver obstruction; stricture; primary biliary cirrhosis;
 KW primary sclerosing cholangitis; colon cancer; therapy; mouse; elf;
 KW embryonic liver fodrin; beta spectrin; epitope.

XX Mus musculus.

PN US2004142354-A1.

XX 22-JUL-2004.

PF 30-OCT-2003; 2003US-00695994.

XX 30-APR-1997; 97US-00841349.

PR 30-APR-1998; 98MO-US008656.

PR 01-NOV-1999; 99US-00431184.

XX (MISH/) MISHRA L.

XX Mishra L;

DR WPI; 2004-552558/53.

PT Novel isolated early liver developmental proteins such as elf, 11yor-1
 (145), pk, protein 106 and praja-1, useful for treating end stage liver
 PT disease, hepatocellular carcinoma, anemia and ataxia.
 XX
 PS Example 2; Page 17; 85pp; English.

XX The invention provides novel early liver developmental proteins such as
 CC elf (embryonic liver fodrin or beta spectrin) 1-3, 11yor-1 (145), pk,
 CC protein 106 and praja-1 and nucleic acid molecules encoding such
 CC proteins. Other genes coding for early liver developmental proteins
 CC include genes 20, 36, 41, 112, 114, 118 and 129. Polynucleotides of the
 CC invention are useful for treating diseases chosen from end stage liver
 CC disease, hepatocellular carcinoma, anhidrotic ectoderm dysplasia,
 CC degenerative neurological disorder, anaemia, ataxia, haemochromatosis,
 CC sideroblastic anaemia and spinocerebellar ataxia. elf sequences are
 CC useful for treating liver disorders chosen from cholestasis, biliary
 CC stones, liver obstruction, stricture, primary biliary cirrhosis and
 CC primary sclerosing cholangitis. praja-1 sequences are useful for
 CC detecting colon cancer. The present sequence is mouse elf-3 epitope
 CC peptide.
 CC
 SO Sequence 15 AA;

Query Match 6.8%; Score 15; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 FNSRRTASDHWSGSM 220
 DB 1 FNSRRTASDHWSGSM 15

RESULT 25

ADV13561
 ID ADV13561 standard; peptide; 17 AA.

XX ADV13561;

DT 10-MAR-2005 (first entry)

DE Human phosphorylated peptide from phosphoprotein #1499.

XX Alzheimer's disease; neuroprotective; nootropic; degeneration; tumor;
 KW neoplasm; neurological disease; phosphorylation; protein sequencing;
 KW phosphoprotein.
 KW
 XX Homo sapiens.

OS

PN WO2004108948-A2.

XX 16-DEC-2004.

PD 04-JUN-2004; 2004WO-US017613.

XX 04-JUN-2003; 2003US-0476010P.

XX (HARD) HARVARD COLLEGE.

XX Gylt SP;

PI WPI; 2005-031720/03.

DR Characterizing phosphorylated polypeptides in a sample comprises
 XX digesting the polypeptides with a protease thus generating test peptides,
 XX and collecting a fraction of test peptides that enriched for positively
 PT charged peptides.
 XX
 PS Claim 16; Page 87; 123pp; English.

XX The invention relates to characterizing phosphorylated polypeptides in a
 CC sample comprising digesting the polypeptides with a protease thus
 CC generating test peptides, and collecting a fraction of test peptides that
 CC enriched for positively charged peptides. Also included are a method
 CC (comprising determining the presence, absence or level of one or more
 CC phosphorylated peptides as identified above in cells having a cell state
 CC and determining the degree of correlation between the presence, absence
 CC or level of phosphorylated polypeptide with the cell state), an isolated
 CC peptide of 5-50 amino acids comprising an amino acid sequence that is a
 CC subsequence of any of the protein sequences given in the specification
 CC (and which comprise a phosphorylation site within the subsequence), an
 CC isolated polypeptide selected from any of the polypeptides listed in the
 CC specification and is modified at a modification site, an isolated peptide
 CC comprising a mass spectral peak signatures. a method for identifying a
 CC treatment that modulates phosphorylation of an amino acid in a target
 CC polypeptide, a method for generating a peptide standard, a pair of
 CC peptide standards comprising the peptide obtained (where the peptide is
 CC phosphorylated and a corresponding peptide comprising an identical amino
 CC acid sequence but which is not phosphorylated), a system (comprising a
 CC computer memory comprising data files storing information relating to the
 CC identifying characteristics of positively charged peptides, and a data
 CC analysis module capable of executing instructions for organizing and/or
 CC searching the data files), a computer program product (comprising data
 CC relating to the identifying characteristics of positively charged
 CC peptides and comprising instructions for organizing and/or searching the
 CC data), and a method for identifying N-terminal peptides in a sample. The
 CC method is useful for characterizing phosphorylated polypeptides in a
 CC sample. The present sequence is a peptide from a human phosphoprotein,
 CC containing a phosphorylation site, identified by the method of the
 CC invention.
 CC
 SO Sequence 17 AA;

Query Match 6.8%; Score 15; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;

	Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	178	QVSGNGLPAPGQSPR	192							
Db	3	QVSGNGLPAPGQSPR	17							
RESULT 26										
ID	ADVA13562	standard; peptide; 17 AA.								
XX	ADVA13562;									
AC	ADVA13562;									
XX	10-MAR-2005 (first entry)									
DT	10-MAR-2005 (first entry)									
XX	Human phosphorylated peptide from phosphoprotein #1500.									
DE	Human phosphorylated peptide from phosphoprotein #1500.									
XX	Alzheimers disease; neuroprotective; nocrotic; degeneration; tumor;									
KM	neoplasm; neurological disease; phosphorylation; protein sequencing;									
XX	phosphoprotein.									
OS	Homo sapiens.									
XX	WO2004108948-A2.									
PN	16-DEC-2004.									
PD	16-DEC-2004.									
PF	04-JUN-2004; 2004WO-US017613.									
XX	04-JUN-2003; 2003US-0476010P.									
PR	04-JUN-2003; 2003US-0476010P.									
XX	(HARD) HARVARD COLLEGE.									
PA	(HARD) HARVARD COLLEGE.									
PI	Gygi SP;									
XX	WPI; 2005-031720/03.									
DR	WPI; 2005-031720/03.									
XX										
XX										
PT	Characterizing phosphorylated polypeptides in a sample comprises									
PT	digesting the polypeptides with a protease thus generating test peptides,									
PR	and collecting a fraction of test peptides that enriched for positively									
PT	charged peptides.									
XX										
XX										
PS	Claim 16; Page 87; 123pp; English.									
XX										
CC	The invention relates to characterizing phosphorylated polypeptides in a									
CC	sample comprising digesting the polypeptides with a protease thus									
CC	generating test peptides, and collecting a fraction of test peptides that									
CC	enriched for positively charged peptides. Also included are a method									
CC	(comprising determining the presence, absence or level of one ore more									
CC	phosphorylated peptides as identified above in cells having a cell state									
CC	and determining the degree of correlation between the presence, absence									
CC	or level of phosphorylated polypeptide with the cell state), an isolated									
CC	peptide of 5-50 amino acids comprising an amino acid sequence that is a									
CC	subsequence of any of the protein sequences given in the specification									
CC	(and which comprise a phosphorylation site within the subsequence), an									
CC	isolated polypeptide selected from any of the polypeptides listed in the									
CC	specification and is modified at a modification site, an isolated peptide									
CC	comprising a mass spectral peak signatures. a method for identifying a									
CC	treatment that modulates phosphorylation of an amino acid in a target									
CC	polypeptide, a method for generating a peptide standard, a pair of									
CC	peptide standards comprising the peptide obtained (where the peptide is									
CC	phosphorylated and a corresponding peptide comprising an									

```

CC invention.
XX
SQ Sequence 17 AA;
Query Match 6.8%; Score 15; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 178 QVSONGLPAEQGSPR 192
DB 3 QVSONGLPAEQGSPR 17
RESULT 27
AAW81644
ID AAW81644 standard; peptide; 14 AA.
XX
XX AAW81644;
AC
XX
XX 01-MAR-1999 (first entry)
DE Mouse elf-1 C-terminal peptide used to raise antibody.
XX
XX Elf-1; mouse; liver development; signal transduction; biliary tree;
XX cholestasis; biliary stone; hepatic obstruction; stricture;
XX primary biliary cirrhosis; primary sclerosing cholangitis; therapy;
XX antibody.
OS
XX Mus sp.
XX
XX WO9848827-A1.
XX
XX 05-NOV-1998.
XX
XX 30-APR-1998; 98WO-US008656.
XX
XX 30-APR-1997; 97US-00841349.
XX
XX (MISH/) MISHRA L.
XX
XX Mishra L;
XX
XX WPI; 1999-009382/01.
XX
XX New isolated early liver development genes - used to develop products for
XX treating, e.g. liver disease, hepatocellular carcinoma, degenerative
XX neurological disorders, anaemia, ataxia or haemochromatosis.
XX
XX Claim 29; Page 25; 92pp; English.
XX
XX This peptide corresponds to amino acids 2140-2154 of the mouse elf-1
XX protein (see AAW81638). Claimed peptides (see AAW81643-52) derived from
XX early liver development proteins (see AAW81638-41) of the invention have
XX been used to raise antibodies. It is an object of the invention to
XX provide proteins which are characteristic of early liver development, and
XX to raise antibodies from these proteins which will be useful as markers,
XX and will be useful in methods of identifying such proteins and peptides,
XX tracing hepatocyte lineage, and treating liver disease. Elf-1 is used in
XX a claimed method to treat cholestasis, biliary stones, liver obstruction,
XX stricture, primary biliary cirrhosis and primary sclerosing cholangitis
XX
XX
SQ Sequence 14 AA;
Query Match 6.4%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 206 FNSRRTASDHWSG 219
DB 1 FNSRRTASDHWSG 14
RESULT 28

```

ADP74507
ID ADF74507 standard; peptide; 14 AA.
XX
AC ADF74507;
XX
XX 26-FEB-2004 (first entry)
DE Peptide from the C-terminus of the murine elf 3 protein (SeqID20).
XX
XX murine; mouse; early liver development; end stage liver disease; elf 1-3;
KM liver-1 (145); pk; protein 106; praja-1; hepatocyte lineage; cholestasis;
KM biliary stone; hepatic obstruction; stricture; primary biliary cirrhosis;
KM primary sclerosing cholangitis; gene therapy;
KM anhidrotic ectoderm dysplasia; hepatocellular carcinoma; anaemia; ataxia;
KM neurological disorder; haemochromatosis; hepatotropic; cytosstatic;
KM neuroprotective; anti-anemic; cardiac; antibody.
XX
OS Mus musculus.
XX
PN US6642362-B1.
XX
PD 04-NOV-2003.
XX
PF 01-NOV-1999; 99US-00431184.
XX
PR 30-APR-1997; 97US-00841349.
PR 30-APR-1998; 98WO-US008656.
XX
PA (MISH/) MISHRA L.
XX
PI Mishra L;
PI
PI WPI; 2003-851362/79.
DR
XX
XX
PT New antibodies recognizing early liver development proteins, useful as
PT markers, in identifying peptides and proteins having early liver
PT development characteristics, tracing hepatocyte lineage or treating liver
PT disease.
XX
XX
PS Claim 1; SEQ ID NO 20; 82pp; English.
XX
XX This invention relates to novel genes and encoded proteins thereof,
CC isolated during early liver development that are useful in the diagnosis
CC and treatment of end stage liver disease and other disorders.
CC Specifically, it refers to genes that encode proteins such as elf 1-3,
CC liver-1 (145), pk, protein 106 and praja-1. The present invention
CC describes the characterisation of these early liver development proteins,
CC and also methods to raise peptide specific antibodies that are useful as
CC markers, as well as for tracing hepatocyte lineage. Furthermore, elf
CC proteins 1-3 are useful in treating disorders including cholestasis,
CC biliary stones, hepatic obstruction, stricture, primary biliary cirrhosis
CC or primary sclerosing cholangitis. In addition, through using gene
CC therapy, praja-1, liver-1 (145) and pk can be used to treat anhidrotic
CC ectoderm dysplasia, hepatocellular carcinoma and other diseases including
CC anaemia, ataxia, degenerative neurological disorders and
CC haemochromatosis. Accordingly, these proteins can be described as
CC hepatotropic, cytosstatic, neuroprotective, anti-anemic and cardiac. This
CC peptide sequence is from the C-terminus of the murine elf 3 protein, used
CC to raise rabbit anti-mouse antibodies of the invention. NOTE: This
CC sequence differs from the murine Elf-3 peptide sequence given in example
CC 2.
XX
SQ Sequence 14 AA;
XX
Query Match 6.4%; Score 14; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
ADQ88379
ID ADQ88379 standard; peptide; 14 AA.
XX
XX
AC ADQ88379;
XX
XX 07-OCT-2004 (first entry)
DE Mouse elf epitope peptide #2.
XX
XX
XX Early liver developmental protein; liver disease;
KM hepatocellular carcinoma; anhidrotic ectoderm dysplasia;
KM degenerative neurological disorder; anaemia; ataxia; haemochromatosis;
KM sideroblastic anaemia; spinocerebellar ataxia; cholestasis;
KM biliary stone; liver obstruction; stricture; primary biliary cirrhosis;
KM primary sclerosing cholangitis; colon cancer; therapy; mouse; elf;
KM embryonic liver fodrin; beta spectrin; epitope.
XX
XX
OS Mus musculus.
XX
PN US2004142354-A1.
XX
PD 22-UU-2004.
XX
PF 30-OCT-2003; 2003US-00695994.
XX
PR 30-APR-1997; 97US-00841349.
PR 30-APR-1998; 98WO-US008656.
XX
PA (MISH/) MISHRA L.
XX
PI Mishra L;
PI
PI WPI; 2004-552558/53.
DR
XX
XX
PT Novel isolated early liver developmental proteins such as elf, liver-1
PT (145), pk, protein 106 and praja-1, useful for treating end stage liver
PT disease, hepatocellular carcinoma, anemia and ataxia.
XX
XX
PS Claim 17; SEQ ID NO 20; 85pp; English.
XX
XX The invention provides novel early liver developmental proteins such as
CC elf (embryonic liver fodrin or beta spectrin) 1-3, liver-1 (145), pk,
CC protein 106 and praja-1 and nucleic acid molecules encoding such
CC proteins. Other genes coding for early liver developmental proteins
CC include genes 20, 36, 41, 112, 114, 118 and 129. Polynucleotides of the
CC invention are useful for treating diseases chosen from end stage liver
CC disease, hepatocellular carcinoma, anhidrotic ectoderm dysplasia,
CC degenerative neurological disorders, anaemia, ataxia, haemochromatosis,
CC sideroblastic anaemia and spinocerebellar ataxia. elf sequences are
CC useful for treating liver disorders chosen from cholestasis, biliary
CC stones, liver obstruction, stricture, primary biliary cirrhosis and
CC primary sclerosing cholangitis. praja-1 sequences are useful for
CC detecting colon cancer. The present sequence is mouse elf epitope
CC peptide.
XX
SQ Sequence 14 AA;
XX
Query Match 6.4%; Score 14; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30
ADY65644
ID ADY65644 standard; protein; 597 AA.
XX
XX
AC ADY65644;

XX 02-JUN-2005 (first entry)
DT
XX S. mansoni protein SEQ ID 1062.
DE
XX Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;
KM diagnosis.
XX Schistosoma mansoni.
OS
XX WO2005023979-A2.
PN
XX 17-MAR-2005.
PD
XX 10-SEP-2004; 2004WO-BR000170.
PF
XX 11-SEP-2003; 2003US-0502277P.
PR
XX (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
PA
XX Verjovski-Almeida S, Leite LCC, Farias LP, Miyasato PA, Kawano T;
PI Demarco R, Garcia JCL, Martins EAL, Ho PU, Nascimento ALTO; V;
PI Dias-Neto B, Secubai JC, Menck CFM, Madeira AMB, Rodrigues V;
PI Gargioni C;
XX WPI; 2005-223357/23.
DR
XX New isolated nucleic acid molecule encoding a Schistosoma mansoni
PT protein, useful for as a vaccine or for preventing, diagnosing, or
PT treating Schistosoma mansoni infection.
PT
XX Disclosure; SEQ ID NO 1062; 52bp; English.
PS
XX The invention relates to an isolated nucleic acid molecule encoding a
XX Schistosoma mansoni protein, or its portion which is at least 20 amino
XX acids in length. Also included are an expression vector comprising the
XX nucleic acid operably linked to a promoter, a recombinant cell
XX transformed/transfected with the nucleic acid (or expression vector), an
XX immunogenic composition comprising the nucleic acid in combination with a
XX pharmaceutical adjuvant or carrier, an isolated S. mansoni protein
XX comprising an amino acid sequence encoded by the nucleic acid, an
XX immunogenic composition comprising the isolated S. mansoni protein, an
XX isolated antibody which specifically binds to the isolated S. mansoni
XX protein, a hybridoma cell line which produces the isolated antibody, a
XX method for determining a S. mansoni infection in a subject and a computer
XX readable medium having recorded in it a nucleic acid molecule from S.
XX mansoni genome. The nucleic acid molecule is useful for preventing,
XX diagnosing, or treating S. mansoni infection (schistosomiasis). It can
XX also be used as vaccine against S. mansoni. The present sequence is a
XX Schistosoma mansoni protein of the invention. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences. Also, SEQ ID 2141-2152 are
XX mentioned in the specification but are not included in the sequence
XX listing.
SQ Sequence 597 AA;
Query Match 6.4%; Score 14; DB 9; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 VQKKTFTKWNVSHL 55
DB 64 VQKKTFTKWNVSHL 77

RESULT 31
AAB50652 standard; protein; 2326 AA.
XX AAB50652;
XX AC
XX

DT 19-MAR-2001 (first entry)
XX
XX C. elegans spectrin beta-chain/fodrin protein SEQ ID NO:12.
DE
XX Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
KM protein-protein interaction; identification.
XX
XX Caenorhabditis elegans.
OS
XX WO2000073328-A2.
PN
XX 07-DEC-2000.
PD
XX 02-JUN-2000; 2000WO-BP005108.
PF
XX 01-JUN-1999; 99GB-00012755.
PR
XX (DEVG-) DEVGEN NV.
PA
XX Van Crielinge W, Roelens I, Bogaert T, Vervaeke P;
PI WPI; 2001-016508/02.
PI N-PSDB; AAC90918.
DR
XX Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
PT identifying unknown human cDNAs which encode proteins that interact with
PT the human unc-5C protein.
PS
XX Claim 37; Page 110-118; 246bp; English.
PS
XX The present invention describes 3 variants of human unc-5C cDNAs (unc-
XX 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
XX 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
XX Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
XX protein-protein-interactions between the unc-5 protein and a variety of
XX different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
XX cDNA are useful in methods for identifying compounds which reduce or
XX inhibit the lethal phenotype associated with the expression of the unc-5
XX death domain in yeast. They are also useful in yeast two hybrid
XX experiments for identifying unknown human cDNAs which encode proteins
XX that interact with the human unc-5C protein. AAC90914 to AAC90971 and
XX AAB50646 to AAB50693 represent sequences used in the exemplification of
XX the present invention.
SQ Sequence 2326 AA;
Query Match 6.4%; Score 14; DB 4; Length 2326;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 VQKKTFTKWNVSHL 55
DB 110 VQKKTFTKWNVSHL 123

RESULT 32
ADN23721
ID ADN23721 standard; protein; 2326 AA.
XX
XX ADN23721;
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polypeptide #6374.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polypeptide.

```

XX  Bacteria.
XX
XX  US2003233675-A1.
XX
XX  18-DEC-2003.
XX
XX  20-FEB-2003; 2003US-00369493.
XX
XX  21-FEB-2002; 2002US-0360039P.
XX
XX  (CAOY/) CAO Y.
XX  (HINK/) HINKLE G J.
XX  (SLAT/) SLATER S C.
XX  (CHEN/) CHEN X.
XX  (GOLD/) GOLDMAN B S.
XX
XX  Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX  WPI; 2004-061375/06.
XX
XX  New recombinant DNA construct comprising a promoter positioned to provide
XX  for expression of a polynucleotide encoding a polypeptide from a
XX  microbial source, useful for producing plants with improved properties.
XX
XX  Claim 1; SEQ ID NO 6374; 122pp; English.
XX
XX  The invention relates to a recombinant DNA construct comprising a
XX  promoter functional in a plant cell, where the promoter is positioned to
XX  provide for expression of a polynucleotide encoding a polypeptide from a
XX  microbial source. The invention also relates to a transformed plant
XX  comprising the recombinant DNA construct and a method of producing a
XX  transformed plant having an improved property. The plant is a crop plant
XX  such as maize or soybean. The method of producing a transformed plant
XX  having an improved property comprises transforming a plant with the
XX  recombinant DNA construct and growing the transformed plant, where the
XX  polynucleotide or polypeptide is useful for improving plant properties.
XX  The recombinant DNA construct is useful for producing plants with
XX  improved plant properties, e.g. improved cold, heat or drought tolerance,
XX  tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX  increased resistance to plant disease, better growth rate by modification
XX  of the cell cycle pathway with plant growth regulators, increased rate of
XX  homologous recombination, modified seed oil or protein yield and/or
XX  content, improved yield by modification of carbohydrate, nitrogen or
XX  phosphorus use and/or uptake, by modification of photosynthesis or by
XX  providing improved plant growth and development under at least one stress
XX  condition, improved lignin production or improved galactomannan
XX  production. This sequence represents a bacterial polypeptide used in the
XX  scope of the invention. Note: The sequence data for this patent did not
XX  form part of the printed specification but was obtained in electronic
XX  format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX  Sequence 2326 AA:
XX
XX  Query Match 6.4%; Score 14; DB 8; Length 2326;
XX  Best Local Similarity 100.0%; Pred. No. 0.00036;
XX  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX  42 YOKKFTKXVNSHL 55
XX  |||||||
XX  110 YOKKFTKXVNSHL 123
XX
XX  RESULT 33
XX  ID AEA55025 standard; protein; 385 AA.
XX
XX  AEA55025;
XX
XX  11-AUG-2005 (first entry)
XX
XX  Human actin-cross-linking protein, ACF7, protein fragment, SEQ ID NO: 1.
XX

```

KM	plasma membrane; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
KW	actin-cross-linking protein.
XX	
OS	Homo sapiens.
PN	MO2005052182-A2.
PD	09-JUN-2005.
XX	
PF	25-NOV-2004; 2004MO-11001085.
XX	
PR	26-NOV-2003; 2003US-0524885P.
XX	
PA	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX	
PI	Linial M, Inberg A, Bledi Y;
XX	
DR	WPI; 2005-418017/42.
DR	PIR; 866292.
PT	Characterizing proteins present in a plasma membrane of a cell, useful in identifying diagnostic markers and potential drugs, comprises subjecting a cell to a protease treatment.
XX	
PS	Claim 25; SEQ ID NO 1; 196bp; English.
XX	
CC	The present invention relates to a method of characterizing proteins present in the plasma membrane (PM) of live cells. The proteins of the invention are useful in identifying diagnostic markers and potential drugs. The invention is useful for identifying drugs for diagnosing and treating disorders such as cancer which are associated with abnormal representation of cell surface proteins. The present sequence is human actin-cross-linking protein, ACF7, protein fragment.
CC	
XX	
SO	Sequence 385 AA;
OY	
DB	
42	VQKKFTKWN 52
96	VQKKFTKWN 106
RESULT 34	
AA59242	
ID	AA59242 standard; protein; 897 AA.
XX	
AC	AA59242;
DT	31-MAR-2000 (first entry)
XX	
DE	A rod shortened dystrophin (deltaDyH4).
XX	
KM	Muscular dystrophy; rod domain; adeno-associated virus; AAV;
KW	dystrophin gene; truncated.
XX	
OS	Homo sapiens.
PN	JP1318467-A.
PD	24-NOV-1999.
XX	
PF	08-MAY-1998; 98JP-00142134.
XX	
PR	08-MAY-1998; 98JP-00142134.
XX	
PA	(KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX	(KOKU-) KOKURITSU SHISHIN SHINKAI CENT SOCHO.
DR	WPI; 2000-100771/09.
DR	N-PSDB; AA248571.

XX A gene encoding a shortened dystrophin - useful for the treatment of
PT muscular dystrophy.
XX
XX
PS Disclosure; Page 32-33; 44pp; Japanese.
XX
CC The invention provides a gene for the treatment of muscular dystrophy
CC having at least one rod repeat structure of hinge 1, hinge 4 and rod
CC domain of dystrophin gene and having a base sequence of 4.5 kb. The gene
CC and a gene-introducing medium consisting of an adeno-associated virus
CC (AAV) vector or lentivirus vector containing the rod shortened dystrophin
CC genes can be used for the genetic treatment of muscular dystrophy of low
CC immune reaction. The present sequence represents a rod shortened
CC dystrophin
XX
SQ Sequence 897 AA;

Query Match 5.0%; Score 11; DB 3; Length 897;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKTFTKVN 52
|||
16 VOKTFTKVN 26
Db

RESULT 35
AAVS9241
ID AAVS9241 standard; protein; 900 AA.
XX
XX AAVS9241;
XX
DT 31-MAR-2000 (first entry)
XX
DE A rod shortened dystrophin (deltadysh1).
XX
KW Muscular dystrophy; rod domain; adeno-associated virus; AAV;
XX dystrophin gene; truncated.
XX
OS Homo sapiens.
XX
XX JP11318467-A.
XX
XX 24-NOV-1999.
XX
XX 08-MAY-1998; 98JP-00142134.
XX
XX 08-MAY-1998; 98JP-00142134.
XX
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX
XX
XX WPI; 2000-100771/09.
XX
XX N-PSDB; AAZ48570.
XX
XX A gene encoding a shortened dystrophin - useful for the treatment of
PT muscular dystrophy.
XX
XX Disclosure; Page 26-28; 44pp; Japanese.
XX
CC The invention provides a gene for the treatment of muscular dystrophy
CC having at least one rod repeat structure of hinge 1, hinge 4 and rod
CC domain of dystrophin gene and having a base sequence of 4.5 kb. The gene
CC and a gene-introducing medium consisting of an adeno-associated virus
CC (AAV) vector or lentivirus vector containing the rod shortened dystrophin
CC genes can be used for the genetic treatment of muscular dystrophy of low
CC immune reaction. The present sequence represents a rod shortened
CC dystrophin
XX
SQ Sequence 900 AA;

Query Match 5.0%; Score 11; DB 3; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKTFTKVN 52
|||
16 VOKTFTKVN 26
Db

RESULT 36
AAVS9237
ID AAVS9237 standard; protein; 1092 AA.
XX
XX AAVS9237;
XX
XX
DT 31-MAR-2000 (first entry)
XX
DE A rod shortened dystrophin (deltadyshx2).
XX
KW Muscular dystrophy; rod domain; adeno-associated virus; AAV;
XX dystrophin gene; truncated.
XX
OS Homo sapiens.
XX
XX JP11318467-A.
XX
XX 24-NOV-1999.
XX
XX 08-MAY-1998; 98JP-00142134.
XX
XX 08-MAY-1998; 98JP-00142134.
XX
XX 08-MAY-1998; 98JP-00142134.
XX
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX
XX
XX WPI; 2000-100771/09.
XX
XX N-PSDB; AAZ48566.
XX
XX
XX A gene encoding a shortened dystrophin - useful for the treatment of
PT muscular dystrophy.
XX
XX Claim 8; Page 14-16; 44pp; Japanese.
XX
XX
CC The invention provides a gene for the treatment of muscular dystrophy
CC having at least one rod repeat structure of hinge 1, hinge 4 and rod
CC domain of dystrophin gene and having a base sequence of 4.5 kb. The gene
CC and a gene-introducing medium consisting of an adeno-associated virus
CC (AAV) vector or lentivirus vector containing the rod shortened dystrophin
CC genes can be used for the genetic treatment of muscular dystrophy of low
CC immune reaction. The present sequence represents a rod shortened
CC dystrophin
XX
SQ Sequence 1092 AA;

Query Match 5.0%; Score 11; DB 3; Length 1092;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKTFTKVN 52
|||
16 VOKTFTKVN 26
Db

RESULT 37
AAVS9240
ID AAVS9240 standard; protein; 1201 AA.
XX
XX AAVS9240;
XX
XX
DT 31-MAR-2000 (first entry)
XX
DE A rod shortened dystrophin (deltadyshx3).
XX
KW Muscular dystrophy; rod domain; adeno-associated virus; AAV;
KW dystrophin gene; truncated.

XX OS Homo sapiens.
XX XX JP1318467-A.
XX PN 24-NOV-1999.
XX PD 08-MAY-1998; 98JP-00142134.
XX PF 08-MAY-1998; 98JP-00142134.
XX PR 08-MAY-1998; 98JP-00142134.
XX PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
XX PA (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX DR MPI; 2000-100771/09.
XX DR N-PSDB; AA248569.
XX PT A gene encoding a shortened dystrophin - useful for the treatment of muscular dystrophy.
XX PS Disclosure; Page 26-28; 44pp; Japanese.
XX CC The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. The present sequence represents a rod shortened dystrophin.
XX CC Sequence 1201 AA;
SQ
Query Match 5.0%; Score 11; DB 3; Length 1201;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42 VOKKTFTKWN 52
DB 16 VOKKTFTKWN 26
RESULT 38
AAV59238
ID AAV59238 standard; protein; 1310 AA.
XX AC AAV59238;
XX DT 31-MAR-2000 (first entry)
XX DE A rod shortened dystrophin (deltadySAx11).
XX KM Muscular dystrophy; rod domain; adeno-associated virus; AAV;
XX KW dystrophin gene; truncated.
XX OS Homo sapiens.
XX XX JP1318467-A.
XX PN 24-NOV-1999.
XX PD 08-MAY-1998; 98JP-00142134.
XX PF 08-MAY-1998; 98JP-00142134.
XX PR 08-MAY-1998; 98JP-00142134.
XX PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
XX PA (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX DR MPI; 2000-100771/09.
XX DR N-PSDB; AA248567.
XX PT A gene encoding a shortened dystrophin - useful for the treatment of muscular dystrophy.
XX

XX XX Claim 8; Page 18-21; 44pp; Japanese.
XX CC The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. The present sequence represents a rod shortened dystrophin.
XX CC Sequence 1310 AA;
SQ
Query Match 5.0%; Score 11; DB 3; Length 1310;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42 VOKKTFTKWN 52
DB 16 VOKKTFTKWN 26
RESULT 39
AAV59239
ID AAV59239 standard; protein; 1310 AA.
XX AC AAV59239;
XX DT 31-MAR-2000 (first entry)
XX DE A rod shortened dystrophin (deltadySAH3).
XX KM Muscular dystrophy; rod domain; adeno-associated virus; AAV;
XX KW dystrophin gene; truncated.
XX OS Homo sapiens.
XX XX JP1318467-A.
XX PN 24-NOV-1999.
XX PD 08-MAY-1998; 98JP-00142134.
XX PF 08-MAY-1998; 98JP-00142134.
XX PR 08-MAY-1998; 98JP-00142134.
XX PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
XX PA (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX DR MPI; 2000-100771/09.
XX DR N-PSDB; AA248568.
XX PT A gene encoding a shortened dystrophin - useful for the treatment of muscular dystrophy.
XX PS Claim 8; Page 22-24; 44pp; Japanese.
XX CC The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. The present sequence represents a rod shortened dystrophin.
XX CC Sequence 1310 AA;
SQ
Query Match 5.0%; Score 11; DB 3; Length 1310;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42 VOKKTFTKWN 52

Db 16 VOKKFTKMN 26

|||||

RESULT 40

ID ADN22598 standard; protein, 1355 AA.

AC ADN22598;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #5251.

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

OS Bacteria.

PN US2003233675-A1.

PD 18-DEC-2003.

PF 20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI, 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 5251, 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQL Sequence 1355 AA;

Query Match 5.0%; Score 11; DB 8; Length 1355;

Best Local Similarity 100.0%; Pred. No. 0.2; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 42 VOKKFTKMN 52
79 VOKKFTKMN 89

RESULT 41

ID ADN22599 standard; protein, 1355 AA.

AC ADN22599;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #5252.

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

OS Bacteria.

PN US2003233675-A1.

PD 18-DEC-2003.

PF 20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI, 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 5252, 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

CC Sequence 1355 AA;

Query Match 5.0%; Score 11; DB 8; Length 1355;

Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

42 VQKTFKWN 52
|||
79 VQKTFKWN 89

RESULT 42

AEA24046 standard; protein; 2000 AA.

AEA24046;

11-AUG-2005 (first entry)

Human PRO polypeptide SEQ ID NO 588.

Immune disorder; PRO; Antiinflammatory; Dermatological;

Immunosuppressive; Antiinflammatory; Antiarthritic; Osteopathic;

Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant.

Homo sapiens.

WO2005051988-A2.

09-JUN-2005.

02-MAR-2004; 2004WO-US006460.

03-MAR-2003; 2003US-0451884P.

(GENTH) GENENTECH INC.

Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI;

WPI; 2005-417958/42.

New nucleic acid encoding PRO polypeptide, useful for diagnosing and

treating an immune related disorder, e.g. systemic lupus erythematosus,

rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or

psoriasis.

Disclosure; SEQ ID NO 588; 966pp; English.

The invention relates to an isolated nucleic acid. The polypeptide,

compound or composition, and methods are useful for diagnosing and

treating an immune related disorder, e.g. systemic lupus erythematosus,

rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,

spondyloarthropathies, systemic sclerosis, idiopathic inflammatory

myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,

autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases

including bullous skin diseases, erythema multiforme and contact

dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

42 VQKTFKWN 52
|||
70 VQKTFKWN 80

SEQUENCE

COMPARELSON A

RESULT 43

AAP90373 standard; protein; 3685 AA.

AAP90373;

29-MAR-1992 (first entry)

Sequence encoded by human muscular dystrophy (MD) cDNA.

Dystrophin; muscular dystrophy; probe; antibody; diagnosis; prenatal;

heterozygote; gene therapy; genetic screening; foetal screening.

Homo sapiens.

WO8906286-A.

13-JUL-1989.

16-DEC-1988; 88WO-US004504.

22-DEC-1987; 87US-0036618.

(CHIL-) CHILDRENS MED CENT.

Kunkel LM, Monaco A, Hoffman EP, Koenig M;

WPI; 1989-220587/30.

N-PSDB; AAN90338.

Muscular dystrophy gene - used for prep. of probes, dystrophic

polypeptide and antibodies for diagnosis and therapy of muscular

dystrophy.

Disclosure; Fig 8; 68pp; English.

The inventors claim an MD probe comprising a purified ss NA SQ which

hybridises to at least a part of the MD gene; pure dystrophin (DS)

polypeptide, purified NA encoding DS and antibodies (Ab) to DS. The

probes are equal to or greater than 10b of one of 12 cDNA sequences

deposited as ATCC 58666-57677. The MD gene is human, or a murine Dmd gene

Sequence 3685 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 0.48; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

42 VQKTFKWN 52
|||
16 VQKTFKWN 26

RESULT 44

AAP90290 standard; protein; 3685 AA.

AAP90290;

25-MAR-2003 (revised)

10-JAN-1990 (first entry)

Human Duchenne muscular dystrophy gene.

Duchenne muscular dystrophy; protein deletion; antiserum.

OS Homo sapiens.
XX
XX EP31514-A.
XX
XX PD 06-SEP-1989.
XX
XX PD 03-MAR-1989; 89EP-00302145.
XX
XX PR 04-MAR-1988; 88JP-00051313.
XX
XX PR 21-SEP-1988; 88JP-00237200.
XX
XX (AJIN) AJINOMOTO KK.
XX
XX PI Ishiguro T, Eguuchi C;
XX
XX DR WPI, 1989-257828/36.
XX
XX PR Detecting human Duchenne muscular dystrophy - by assaying for the
XX associated protein deletion or defect using antibody to the protein.
XX
XX PS Claim 3; Page 15-16; 20pp; English.
XX
XX CC Peptides may be prepared consisting of all or part of the sequence and
XX used to produce Abs for detecting protein deletions or defects in the
XX CC Gene. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
XX CC 2003 to correct PA field.)
XX
XX SQ Sequence 3685 AA;

Query Match 5.0%; Score 11; DB 1; Length 3685;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTKWN 52
DB 16 VOKKFTKWN 26

RESULT 45
ADL83110
ID ADL83110 standard; protein; 3685 AA.
XX
XX AC ADL83110;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE Human PRO84704, SEQ ID 312.
XX
XX KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;
XX KW Gene therapy; PRO; B cell related disorder; cancer;
XX KW Immune-mediated inflammatory disease; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004024097-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 15-SEP-2003; 2003WO-US029097.
XX
XX PR 16-SEP-2002; 2002US-0411392P.
XX
XX PA (GERTH) GENENTECH INC.
XX
XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX PI Wu TD;
XX
XX DR WPI, 2004-329389/30.
XX
XX DR N-PSDB; ADL83109.
XX
XX PT New PRO polypeptide, useful for diagnosing and treating a B cell related
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune

PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX PS Claim 10; Fig 312; 695pp; English.
XX
XX CC The present invention relates to PRO proteins and their coding sequences.
XX CC The PRO proteins are useful for diagnosing and treating a B cell related
XX CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
XX CC antigen unresponsiveness, selective IGA deficiency, selective IGM
XX CC deficiency, selective deficiency of Igg subclasses, immunodeficiency with
XX CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
XX CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX CC medicament for treating a condition that is responsive to the PRO
XX CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX CC coding sequences are useful as hybridization probes in chromosome and
XX CC gene mapping, in preparing PRO proteins, or in generating transgenic
XX CC animals or knockout animals, which in turn are useful in the development
XX CC and screening of therapeutically useful reagents.
XX
XX SQ Sequence 3685 AA;

Query Match 5.0%; Score 11; DB 8; Length 3685;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTKWN 52
DB 16 VOKKFTKWN 26

RESULT 46
ADN04004
ID ADN04004 standard; protein; 3685 AA.
XX
XX AC ADN04004;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Antipsoriatic protein sequence #197.
XX
XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
XX OS Homo. sapiens.
XX
XX PN WO2004028479-A2.
XX
XX PD 08-APR-2004.
XX
XX PF 25-SEP-2003; 2003WO-US030907.
XX
XX PR 25-SEP-2002; 2002US-0414006P.
XX
XX PA (GERTH) GENENTECH INC.
XX
XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX PI Wu TD;
XX
XX DR WPI, 2004-305105/28.
XX
XX DR N-PSDB; ADN04003.
XX
XX PT New PRO nucleic acid or polypeptide, useful for preparing a
XX PT pharmaceutical composition for diagnosing or treating psoriasis in a
XX PT mammal.
XX
XX PS Claim 9; SEQ ID NO 398; 306pp; English.
XX
XX CC The invention relates to novel polynucleotide and polypeptides for
XX CC treating psoriasis or a sequence having at least 80% identity to the
XX CC above sequences. The nucleic acid is useful for preparing a composition
XX CC for diagnosing or treating psoriasis in a mammal. This sequence
XX CC corresponds to one of the polypeptides of the invention.

XX Sequence 3685 AA;

Query Match 5.0%; Score 11; DB 8; Length 3685;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VQKTFKTKWN 52
|||
16 VQKTFKTKWN 26

RESULT 47
AAU14603
AAU14603 standard; protein; 5373 AA.

AAU14603;

24-OCT-2001 (first entry)

Novel bone marrow polypeptide #2.

Bone marrow; diagnostic; therapeutic; gene therapy; antigenic;
haematopoiesis; myeloid; lymph cell disorder; tissue regeneration;
wound healing; nutritional supplement; immune disorder;
severe combined immunodeficiency; SCID.

Homo sapiens.

WO200157187-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US003782.

03-FEB-2000; 2000US-00496914.

20-JUN-2000; 2000US-00598075.

19-JUL-2000; 2000US-00620325.

30-NOV-2000; 2000US-0250683P.

(HYSE-) HYSEQ INC.

Ford JF, Boyle BJ, Tang YT, Liu C, Asundi V, Zhou P, Xue AJ;

Ren F, Drmanac RT;

WPI: 2001-488875/53.

N-PSDB; AAS22908.

Nucleic acids encoding bone marrow polypeptides, useful in diagnostic and

gene therapy.

Claim 10; Page 198-208; 392pp; English.

AAU14603-AAU14794 represent novel bone marrow polypeptides of the
invention. The proteins and corresponding coding sequences may be used in
the prevention, diagnosis and treatment of diseases associated with
inappropriate bone marrow polypeptide expression. For example, to treat
disorders associated with decreased expression by rectifying mutations or
deletions in a patient's genome that affect the activity of the
polypeptides by expressing inactive proteins or to supplement the
patient's own production of the polypeptides. Additionally, the nucleic
acids may be used to produce the polypeptides, by inserting the nucleic
acids into a host cell and culturing the cell to express the protein. The
nucleic acid and its complementary sequences may also be used as DNA
probes in diagnostic assays to detect and quantitate the presence of
similar nucleic acid sequences in samples, and therefore which patients
may be in need of restorative therapy. The proteins may also be used as
antigens in the production of antibodies against bone marrow proteins and
in assays to identify modulators of their expression and activity. The
anti-bone marrow protein antibodies and antagonists may also be used to
down regulate expression and activity. The antibodies may also be used as
diagnostic agents for detecting the presence of the protein in samples
(e.g. by enzyme linked immunosorbant assay (ELISA)). The proteins may be

used to regulate hematopoiesis activity, and consequently in the
treatment of myeloid or lymph cell disorders; in tissue regeneration, of
such as wound healing; as a nutritional supplement; and in treatment of
immune disorders such as severe combined immunodeficiency (SCID)

Sequence 5373 AA;

Query Match 5.0%; Score 11; DB 4; Length 5373;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VQKTFKTKWN 52
|||
44 VQKTFKTKWN 54

RESULT 48
ADU68935
ADU68935 standard; protein; 5373 AA.

ADU68935;

06-MAY-2004 (first entry)

Human heat mitochondrial protein as a therapeutic target SegID741.

mitochondrial; human; screening assay; diabetes mellitus;

Huntington's disease; osteoarthritis;

Leber's hereditary optic neuropathy; LHON;

mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

myoclonic epilepsy ragged red fibre syndrome; MERFP; cancer;

neuroprotective; noctropic; antidiabetic; anticonvulsant; antiarthritic;

osteopathic; ophthalmological; cyostatic.

Homo sapiens.

WO2003087768-A2.

23-OCT-2003.

04-APR-2003; 2003WO-US010870.

12-APR-2002; 2002US-0372843P.

17-JUN-2002; 2002US-038987P.

20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR.

(BUCK-) BUCK INST AGE RES.

Ghoosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;

WPI: 2003-845369/78.

Claim 1; SEQ ID NO 741; 180pp; English.

This invention relates to novel mitochondrial targets that can be used
for therapeutic intervention in treating a disease associated with
altered mitochondrial function. Specifically, it refers to a method for
identifying proteins of the human heart mitochondrial proteome that are
useful for drug screening assays, as well as therapeutic targets. The
present invention describes a method for identifying such proteins that
can be used in the treatment of various diseases associated with altered
mitochondrial function including diabetes mellitus, Huntington's disease,
osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
ragged red fibre syndrome (MERFP) or cancer. Accordingly, these
compositions have neuroprotective, noctropic, antidiabetic,

CC anti-contractant, antiarthritic, osteopathic, ophthalmological and
CC cytoskeletal activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 5373 AA;

Query Match 5.0%; Score 11; DB 7; Length 5373;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTFKWN 52
|||
44 VOKKFTFKWN 54

RESULT 49

ID AD285102 standard; protein; 5430 AA.

XX AD285102;

DT 14-JUL-2005 (first entry)

DE Full-length FOS interacting protein, SEQ ID 151.

XX FOS; anti-inflammatory; neuroprotective; cytoskeletal; cardiovascular-Gen.;
XX anti-diabetic; inflammation; neurodegenerative disease; cancer;

KM cardiovascular disease; diabetes mellitus.

XX Homo sapiens.

PN US2005100966-A1.

PD 12-MAY-2005.

PF 19-MAR-2004; 2004US-00805684.

PR 02-APR-2003; 2003US-0459936P.

PR 02-APR-2003; 2003US-0460103P.

PR 03-JUN-2003; 2003US-0455766P.

XX (SAKA/) SAKAMOTO T.

PA (TAKE/) TAKEDA S.

PI Sakamoto T, Takeda S;

DR WPI; 2005-345401/35.

PT Novel isolated protein comprising FOS or its homolog, derivative or
PT fragment, interacting with proteins chosen from group of GROUP1 e.g.
PT MKRP23, MKRP5 or MKRD7(627), useful for screening its modulator.

PS Disclosure; SEQ ID NO 151; 163pp; English.

XX The invention relates to a novel isolated protein comprising a first
CC protein, which is FOS or its homolog, derivative or fragment,
CC interacting with a second protein chosen from a group of GROUP1, e.g.
CC MKRP23, MKRP5 or MKRD7(627), where the interaction is through a complex
CC or covalent bond, or any other intermolecular interaction. The invention
CC further comprises: a method for producing the FOS-interacting protein; a
CC method for detecting the FOS-interacting protein in a sample; a method
CC for determining whether a compound is capable of modulating an
CC interaction between a first polypeptide (FOS) or its homolog, derivative
CC of fragment) and a second polypeptide as mentioned in the FOS-
CC interacting protein; and a method for modulating the function or activity
CC of the FOS-interacting protein in cells of a specific tissue of a
CC mammal. The FOS-interacting protein has the activities:
CC anti-inflammatory, neuroprotective, cytoskeletal, cardiovascular-Gen., and
CC anti-diabetic. The FOS-interacting protein is useful for selecting its
CC modulators. The method for modulating the function or activity of the
CC FOS-interacting protein in cells of a specific tissue is useful for
CC treating inflammatory diseases, neurodegenerative diseases, cancer,
CC cardiovascular diseases or diabetes mellitus. This sequence represents an

CC FOS interacting protein for use in the novel protein complex of the
CC invention.

XX Sequence 5430 AA;

Query Match 5.0%; Score 11; DB 9; Length 5430;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTFKWN 52
|||
79 VOKKFTFKWN 89

RESULT 50

ID AAU14697 standard; protein; 5447 AA.

XX AAU14697;

DT 24-OCT-2001 (first entry)

DE Novel bone marrow polypeptide #96.

XX Bone marrow; diagnostic; therapeutic; gene therapy; antigenic;
XX haematopoiesis; myeloid; lymph cell disorder; tissue regeneration;
XX wound healing; nutritional supplement; immune disorder;

KM severe combined immunodeficiency; SCID.

XX Homo sapiens.

PN WO200157187-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US003782.

PR 03-FEB-2000; 2000US-00496914.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 30-NOV-2000; 2000US-0250683P.

XX (HYSE-) HYSEQ INC.

PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Zhou P, Xue AJ,

PI Ren F, Drmanac RT;

DR WPI; 2001-488875/53.

DR N-PSDB; AAS23002.

PT Nucleic acids encoding bone marrow polypeptides, useful in diagnostic and
PT gene therapy.

PS Claim 10; Page 124-127; 392pp; English.

XX AAU14602-AAU14794 represent novel bone marrow polypeptides of the
CC invention. The proteins and corresponding coding sequences may be used in
CC the prevention, diagnosis and treatment of diseases associated with
CC inappropriate bone marrow polypeptide expression. For example, to treat
CC disorders associated with decreased expression by rectifying mutations or
CC deletions in a patient's genome that affect the activity of the
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of the polypeptides. Additionally, the nucleic
CC acids may be used to produce the polypeptides, by inserting the nucleic
CC acids into a host cell and culturing the cell to express the protein. The
CC nucleic acid and its complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acid sequences in samples, and therefore which patients
CC may be in need of restorative therapy. The proteins may also be used as
CC antigens in the production of antibodies against bone marrow proteins and
CC in assays to identify modulators of their expression and activity. The
CC anti-bone marrow protein antibodies and antagonists may also be used to
CC down regulate expression and activity. The antibodies may also be used as

CC diagnostic agents for detecting the presence of the protein in samples
 CC (e.g. by enzyme linked immunosorbant assay (ELISA)). The proteins may be
 CC used to regulate haematopoiesis activity, and consequently in the
 CC treatment of myeloid or lymph cell disorders; in tissue regeneration,
 CC such as wound healing; as a nutritional supplement; and in treatment of
 CC immune disorders such as severe combined immunodeficiency (SCID)
 XX

SQ Sequence 5447 AA;

Query Match 5.0%; Score 11; DB 4; Length 5447;

Best Local Similarity 100.0%; Pred. NO. 0.67; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKTFTKWN 52
 |||||
 Db 96 VOKKTFTKWN 106

Search completed: March 4, 2006, 07:06:15
 Job time : 242 secs

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OM protein - protein search, using SW model

Run on: March 4, 2006, 07:02:16 ; Search time 230 Seconds
(without alignments)
674.853 Million cell updates/sec

Title: US-10-695-994A-7
Perfect score: 220
Sequence: 1 MELORTSSISGPLSPATYGTQ.....QNYKNFNSRTASHDSWGM 220

Scoring table: @MGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 8624

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt.05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	220	Q922V0_MOUSE	Q922V0 mus musculus
2	133	60.5	155	Q8C509_MOUSE	Q8C509 mus musculus
3	133	60.5	2154	Q5S0L9_MOUSE	Q5S0L9 mus musculus
4	133	60.5	2155	Q81X99_HUMAN	Q81X99 homo sapien
5	124	56.4	2154	Q9QWJ7_MOUSE	Q9QWJ7 mus musculus
6	97	44.1	149	Q6V0G7_CANFA	Q6V0G7 canis famli
7	97	44.1	1290	Q5DTR4_MOUSE	Q5DTR4 mus musculus
8	97	44.1	2358	Q6XD99_RAT	Q6XD99 rattus norv
9	97	44.1	2363	SPTB2_MOUSE	SPTB2 mus musculus
10	97	44.1	2363	Q5S0L8_MOUSE	Q5S0L8 mus musculus
11	97	44.1	2364	SPTB2_HUMAN	SPTB2 homo sapien
12	97	44.1	2377	Q59ER3_HUMAN	Q59ER3 homo sapien
13	96	43.6	2314	Q53R99_HUMAN	Q53R99 homo sapien
14	66	30.0	977	Q502M3_BRARE	Q502M3 brachydanio
15	65	29.5	2235	Q4REK5_TETNG	Q4REK5 tetractodon n
16	62	28.2	332	Q9QWJ7_MOUSE	Q9QWJ7 mus sp. bet
17	62	28.2	497	Q8BQJ3_MOUSE	Q8BQJ3 mus musculus
18	60	27.3	97	Q8V165_RAT	Q8V165 rattus norv
19	48	21.8	48	Q9RLY9_MOUSE	Q9RLY9 mus musculus
20	47	21.4	2275	Q4SR66_TETNG	Q4SR66 tetractodon n
21	46	20.9	2307	Q4SVU8_TETNG	Q4SVU8 tetractodon n
22	46	20.9	2357	Q9DGM6_BRARE	Q9DGM6 brachydanio
23	38	17.3	2127	SPTB1_MOUSE	SPTB1 mus musculus
24	38	17.3	2136	SPTB1_HUMAN	SPTB1 homo sapien
25	38	17.3	2137	Q6XDA0_RAT	Q6XDA0 rattus norv
26	38	17.3	2332	Q59RPS_HUMAN	Q59RPS homo sapien
27	37	16.8	67	Q8RTB3_HUMAN	Q8RTB3 homo sapien
28	37	16.8	82	Q9WUX0_RAT	Q9WUX0 rattus norv
29	32	14.5	516	Q5D002_RAT	Q5D002 rattus norv
30	28	12.7	2413	Q4SF10_TETNG	Q4SF10 tetractodon n
31	27	12.3	794	Q5XG36_XENILA	Q5XG36 xenopus lae

32	27	12.3	1060	Q7ZX11_XENILA	Q7ZX11 xenopus lae
33	27	12.3	2388	SPTN2_RAT	SPTN2 rattus norv
34	27	12.3	2388	Q68FG2_MOUSE	Q68FG2 mus musculus
35	27	12.3	2390	SPTN2_HUMAN	SPTN2 homo sapien
36	25	11.0	51	Q71VG2_HUMAN	Q71VG2 homo sapien
37	22	10.0	2002	Q71S06_HUMAN	Q71S06 homo sapien
38	22	10.0	2555	Q91Z66_MOUSE	Q91Z66 mus musculus
39	22	10.0	2561	Q8V1E5_MOUSE	Q8V1E5 mus musculus
40	22	10.0	2564	SPTN4_HUMAN	SPTN4 homo sapien
41	22	10.0	2564	Q71S07_HUMAN	Q71S07 homo sapien
42	19	8.6	1410	Q6NNX2_DROME	Q6NNX2 drosophila
43	19	8.6	2291	SPTC8_DROME	SPTC8 drosophila
44	17	7.7	20	Q9TR82_PIG	Q9TR82 sus scrofa
45	16	7.3	707	Q28297_CANFA	Q28297 canis famli
46	16	7.3	2296	Q2PSH4_ANOGA	Q2PSH4 anophles g
47	15	6.8	129	Q4RFW3_TETNG	Q4RFW3 tetractodon n
48	14	6.4	2257	Q9U9J7_MOUSE	Q9U9J7 caenorhabdi
49	14	6.4	2299	Q6WPE8_CAEBL	Q6WPE8 caenorhabdi
50	14	6.4	2302	Q95ZL8_CAEBL	Q95ZL8 caenorhabdi
51	14	6.4	2302	Q9U9J8_MOUSE	Q9U9J8 caenorhabdi
52	14	6.4	2339	Q961X7_BRUMA	Q961X7 briglia mala
53	13	5.9	373	Q4SR67_TETNG	Q4SR67 tetractodon n
54	12	5.5	1315	Q4S2Y7_TETNG	Q4S2Y7 tetractodon n
55	12	5.5	3641	Q7ZTH4_FUGRU	Q7ZTH4 fuigu rubrip
56	11	5.0	20	Q8WYF6_HUMAN	Q8WYF6 homo sapien
57	11	5.0	41	Q5JXB4_HUMAN	Q5JXB4 homo sapien
58	11	5.0	50	Q8WXY4_HUMAN	Q8WXY4 homo sapien
59	11	5.0	65	Q81OC9_RAT	Q81OC9 rattus norv
60	11	5.0	101	Q14172_HUMAN	Q14172 homo sapien
61	11	5.0	108	Q8C221_MOUSE	Q8C221 mus musculus
62	11	5.0	256	Q816B6_DROME	Q816B6 drosophila
63	11	5.0	385	Q13696_HUMAN	Q13696 homo sapien
64	11	5.0	420	Q516R1_ENTHI	Q516R1 entameoba h
65	11	5.0	440	Q5R9D0_PONPY	Q5R9D0 pongo pygma
66	11	5.0	462	Q6PK12_HUMAN	Q6PK12 homo sapien
67	11	5.0	470	Q5R8S0_PONPY	Q5R8S0 pongo pygma
68	11	5.0	565	Q8BTW7_ENCCU	Q8BTW7 encephalito
69	11	5.0	676	Q8C8S5_MOUSE	Q8C8S5 mus musculus
70	11	5.0	719	Q5JXW4_HUMAN	Q5JXW4 homo sapien
71	11	5.0	772	Q5JXQ4_HUMAN	Q5JXQ4 homo sapien
72	11	5.0	786	Q503P9_BRARE	Q503P9 brachydanio
73	11	5.0	964	PLEC1_MOUSE	Q9QX81 mus musculus
74	11	5.0	1375	Q4RUK6_TETNG	Q4RUK6 tetractodon n
75	11	5.0	1445	Q4SY67_TETNG	Q4SY67 tetractodon n
76	11	5.0	1454	Q7ZMK4_XENILA	Q7ZMK4 xenopus lae
77	11	5.0	1697	Q4SY99_TETNG	Q4SY99 tetractodon n
78	11	5.0	3322	Q6BEO3_CAEBL	Q6BEO3 caenorhabdi
79	11	5.0	3323	Q6BEO4_CAEBL	Q6BEO4 caenorhabdi
80	11	5.0	3405	Q6BEO5_CAEBL	Q6BEO5 caenorhabdi
81	11	5.0	3436	Q6BEP8_CAEBL	Q6BEP8 caenorhabdi
82	11	5.0	3436	Q6BEP9_CAEBL	Q6BEP9 caenorhabdi
83	11	5.0	3436	Q18290_CAEBL	Q18290 caenorhabdi
84	11	5.0	3522	Q86NF7_CAEBL	Q86NF7 caenorhabdi
85	11	5.0	3680	DMD_CANFA	Q97592 canis famli
86	11	5.0	3685	DMD_HUMAN	P11532 homo sapien
87	11	5.0	3685	Q7KZ48_HUMAN	Q7KZ48 homo sapien
88	11	5.0	3685	Q5JYU0_HUMAN	Q5JYU0 homo sapien
89	11	5.0	4410	Q6EUT7_CAEBL	Q6EUT7 caenorhabdi
90	11	5.0	4511	Q6S388_MOUSE	Q6S388 mus musculus
91	11	5.0	4513	Q6S399_RAT	Q6S399 rattus norv
92	11	5.0	4515	Q6S379_HUMAN	Q6S379 homo sapien
93	11	5.0	4521	Q6S392_MOUSE	Q6S392 mus musculus
94	11	5.0	4523	Q6S3A3_RAT	Q6S3A3 rattus norv
95	11	5.0	4525	Q6S3B1_HUMAN	Q6S3B1 homo sapien
96	11	5.0	4533	Q6S382_HUMAN	Q6S382 homo sapien
97	11	5.0	4534	Q6S393_MOUSE	Q6S393 mus musculus
98	11	5.0	4536	Q6S3A4_RAT	Q6S3A4 rattus norv
99	11	5.0	4543	Q6S384_MOUSE	Q6S384 mus musculus
100	11	5.0	4543	Q6S387_MOUSE	Q6S387 mus musculus
101	11	5.0	4545	Q6S395_RAT	Q6S395 rattus norv
102	11	5.0	4545	Q6S398_RAT	Q6S398 rattus norv
103	11	5.0	4547	Q6S376_HUMAN	Q6S376 homo sapien
104	11	5.0	4547	Q6S378_HUMAN	Q6S378 homo sapien

105	11	5.0	4550	2	066385 MOUSE	066385 mus musculus	178	8	3.6	440	2	050NF1_ENTHI	050NF1 entamoeba h
106	11	5.0	4551	2	066377 HUMAN	066377 homo sapien	179	8	3.6	457	2	050X88_ENTHI	050X88 entamoeba h
107	11	5.0	4552	2	066396 RAT	066396 rattus norv	180	8	3.6	472	2	04RQUT_TETNG	04RQUT tetraodon n
108	11	5.0	4572	2	066394 MOUSE	066394 mus musculus	181	8	3.6	484	2	050W17_ENTHI	050W17 entamoeba h
109	11	5.0	4574	2	066383 HUMAN	066383 homo sapien	182	8	3.6	482	2	050Z94_ENTHI	050Z94 entamoeba h
110	11	5.0	4574	2	066345 RAT	066345 rattus norv	183	8	3.6	534	2	0518F3_ENTHI	0518F3 entamoeba h
111	11	5.0	4684	2	066380 HUMAN	066380 homo sapien	184	8	3.6	534	2	04RNG2_TETNG	04RNG2 tetraodon n
112	11	5.0	4686	2	066389 MOUSE	066389 mus musculus	185	8	3.6	572	2	04W116_ASPFU	04W116 aspergillus
113	11	5.0	4688	2	066340 RAT	066340 rattus norv	186	8	3.6	592	2	004096_ARATH	004096 arabidopsis
114	11	5.0	4944	2	07K7B8_CABEL	07K7B8 caenorhabdi	187	8	3.6	599	2	07T3H6_BRARE	07T3H6 brachydantio
115	11	5.0	4955	2	0867D9_CABEL	0867D9 caenorhabdi	188	8	3.6	605	2	0514P9_ENTHI	0514P9 entamoeba h
116	11	5.0	4955	2	0867D9_CABEL	0867D9 caenorhabdi	189	8	3.6	619	2	050SC7_ENTHI	050SC7 entamoeba h
117	11	5.0	5327	1	MACF1_MOUSE	094XZ0 mus musculus	190	8	3.6	737	2	0571A0_MOUSE	0571A0 mus musculus
118	11	5.0	5430	2	MACF1_MOUSE	094XZ0 mus musculus	191	8	3.6	737	2	PDCC8_DROME	PDCC8 drome
119	11	5.0	5430	2	MACF1_MOUSE	094XZ0 mus musculus	192	8	3.6	762	2	050RA3_ENTHI	050RA3 entamoeba h
120	11	5.0	5430	2	MACF1_MOUSE	094XZ0 mus musculus	193	8	3.6	762	2	080016_FUGRU	080016 fugu rubrip
121	10	4.5	1844	2	05BDW2_EBENI	05BDW2 aspergillus	194	8	3.6	822	2	09NSP5_CABEL	09NSP5 caenorhabdi
122	10	4.5	1844	2	05BDW2_EBENI	05BDW2 aspergillus	195	8	3.6	822	2	06DE51_XENLA	06DE51 xenopus lae
123	10	4.5	2285	2	07KAJ2_DROME	07KAJ2 drosophila	196	8	3.6	857	2	050UD2_ENTHI	050UD2 entamoeba h
124	10	4.5	2396	2	077291_DROME	077291 drosophila	197	8	3.6	857	2	051GH3_ENTHI	051GH3 entamoeba h
125	10	4.5	5201	2	07KJN6_DROME	07KJN6 drosophila	198	8	3.6	858	2	P90545_ENTHI	P90545 entamoeba h
126	10	4.5	5201	2	08ML80_DROME	08ML80 drosophila	199	8	3.6	887	2	04PA36_USITMA	04PA36 uetillago ma
127	10	4.5	5301	2	09V6V3_DROME	09V6V3 drosophila	200	8	3.6	889	2	04RZ26_TETNG	04RZ26 tetraodon n
128	10	4.5	5390	2	09V6V4_DROME	09V6V4 drosophila	201	8	3.6	890	2	06NRW6_XENLA	06NRW6 xenopus lae
129	10	4.5	5501	2	09V6V2_DROME	09V6V2 drosophila	202	8	3.6	890	2	06P0U5_BRARE	06P0U5 brachydantio
130	10	4.1	5501	2	0811A1_9MURI	0811A1 mus sp. dys	203	8	3.6	892	2	062744_RAT	062744 rattus norv
131	9	4.1	47	2	05THP1_HUMAN	05THP1 homo sapien	204	8	3.6	894	1	ACTN2_HUMAN	ACTN2 human
132	9	4.1	99	2	063770_9MURI	063770 rattus sp.	205	8	3.6	894	1	ACTN2_MOUSE	ACTN2 mouse
133	9	4.1	107	2	063771_9MURI	063771 rattus sp.	206	8	3.6	894	2	05VXF1_HUMAN	05VXF1 human
134	9	4.1	124	2	04ROA6_TETNG	04ROA6 tetraodon n	207	8	3.6	894	2	05FW75_MOUSE	05FW75 mouse
135	9	4.1	153	2	05SYX1_HUMAN	05SYX1 homo sapien	208	8	3.6	894	2	06RKQ4_MOUSE	06RKQ4 mouse
136	9	4.1	269	2	08C7R5_MOUSE	08C7R5 mus musculus	209	8	3.6	894	2	06DF05_XENTR	06DF05 xenopus tro
137	9	4.1	292	1	TNNI_CHTNT	07M3Y3 chlamys ntp	210	8	3.6	894	2	06IP14_XENLA	06IP14 xenopus lae
138	9	4.1	293	2	015988_PATYE	015988 patinopecte	211	8	3.6	896	2	06DFU3_XENLA	06DFU3 xenopus lae
139	9	4.1	314	2	015987_PATYE	015987 patinopecte	212	8	3.6	896	2	07SYD3_BRARE	07SYD3 brachydantio
140	9	4.1	541	2	06YBR7_BRARE	06YBR7 brachydantio	213	8	3.6	896	2	06TNW2_BRARE	06TNW2 brachydantio
141	9	4.1	589	2	05RCK8_PONPY	05RCK8 pongo pygma	214	8	3.6	897	1	ACTN2_CHICK	ACTN2 chick
142	9	4.1	603	2	09VOM7_PYRAB	09VOM7 pyrococcus	215	8	3.6	897	2	04ST30_TETNG	04ST30 tetraodon n
143	9	4.1	603	2	04IFB4_GIBZE	04IFB4 gibberella	216	8	3.6	898	2	08AX99_BRARE	08AX99 brachydantio
144	9	4.1	633	2	04IFB0_GIBZE	04IFB0 gibberella	217	8	3.6	904	2	07SYE2_BRARE	07SYE2 brachydantio
145	9	4.1	689	2	05T0V7_HUMAN	05T0V7 homo sapien	218	8	3.6	904	1	ACTN4_CHICK	ACTN4 chick
146	9	4.1	732	2	0810I5_MOUSE	0810I5 mus musculus	219	8	3.6	904	2	06DCS6_XENLA	06DCS6 xenopus lae
147	9	4.1	732	2	06PEL2_MOUSE	06PEL2 mus musculus	220	8	3.6	904	2	06DPF7_XENTR	06DPF7 xenopus tro
148	9	4.1	874	2	018109_CABEL	018109 caenorhabdi	221	8	3.6	911	1	ACTN4_HUMAN	ACTN4 human
149	9	4.1	1086	2	05ZME3_CHICK	05ZME3 gallus gall	222	8	3.6	911	2	ACTN4_RAT	ACTN4 rat
150	9	4.1	1304	2	09PWF6_MORSA	09PWF6 morone saxa	223	8	3.6	911	2	05RCS6_PONPY	05RCS6 pongo pygma
151	9	4.1	1678	1	BPABR_MOUSE	060824 mus musculus	224	8	3.6	912	2	06P786_RAT	06P786 rattus norv
152	9	4.1	2063	2	046B73_DROME	046B73 drosophila	225	8	3.6	912	1	ACTN4_MOUSE	ACTN4 mouse
153	9	4.1	3029	2	046B73_DROME	046B73 drosophila	226	8	3.6	918	2	05LJPI_DROME	05LJPI drome
154	9	4.1	3214	1	BPAL_HUMAN	003001 homo sapien	227	8	3.6	965	2	05H724_FUGRU	05H724 fugu rubrip
155	9	4.1	3419	2	055147_RAT	055147 rattus norv	228	8	3.6	1011	1	PERO1_MOUSE	PERO1 mouse
156	9	4.1	3429	2	008614_MOUSE	008614 mus musculus	229	8	3.6	1035	2	0677W7_HUMAN	0677W7 human
157	9	4.1	3432	2	05JCF5_CANFA	05JCF5 canis famli	230	8	3.6	1043	2	0617W8_MOUSE	0617W8 mouse
158	9	4.1	3433	1	UTRO_HUMAN	046939 homo sapien	231	8	3.6	1089	2	05X908_STRCO	05X908 strepto
159	9	4.1	3543	2	05S2S7_HUMAN	05S2S7 homo sapien	232	8	3.6	1172	2	07R3O6_GIALA	07R3O6 giardia lam
160	9	4.1	3543	2	07T1P2_FUGRU	07T1P2 fugu rubrip	233	8	3.6	1190	2	09HS95_HALSA	09HS95 halobacteri
161	9	4.1	3660	1	DMD_CHICK	07L1D2 gallus gall	234	8	3.6	1253	2	0729R3_DESVH	0729R3 desulfovibr
162	9	4.1	3674	1	DMD_MOUSE	07L1D2 gallus gall	235	8	3.6	1462	2	04SXZ7_TETNG	04SXZ7 tetraodon n
163	9	4.1	3678	1	DMD_MOUSE	07L1D2 gallus gall	236	8	3.6	1462	2	07Z6C1_HUMAN	07Z6C1 homo sapien
164	9	4.1	5457	1	BPAL_MOUSE	05TBT1 human	237	8	3.6	1609	2	07RYS2_NEUCR	07RYS2 neurospora
165	9	4.1	7389	1	BPAL_MOUSE	05TBT1 human	238	8	3.6	1645	2	099140_DROME	099140 drosophila
166	9	4.1	7543	1	BPAL_MOUSE	05TBT1 human	239	8	3.6	1648	2	06FSR4_CANGA	06FSR4 candida gla
167	9	4.1	7543	1	BPAL_MOUSE	05TBT1 human	240	8	3.6	1738	2	051ED7_ENTHI	051ED7 entamoeba h
168	8	3.6	107	2	061063_MOUSE	061063 mus musculus	241	8	3.6	1843	2	04RRAB_TETNG	04RRAB tetraodon n
169	8	3.6	110	2	08A9W5_SALSA	08A9W5 salmo salar	242	8	3.6	1843	2	096819_CABEL	096819 caenorhabdi
170	8	3.6	169	2	072RH4_LEPIC	072RH4 lepicospira	243	8	3.6	1846	2	016131_CABEL	016131 caenorhabdi
171	8	3.6	169	2	08FA93_LEPIC	08FA93 lepicospira	244	8	3.6	2053	2	0694W8_XENIA	0694W8 xenopus lae
172	8	3.6	246	2	07XP04_ORISA	07XP04 cryza sativ	245	8	3.6	2221	2	07S3C3_NEUCR	07S3C3 neurospora
173	8	3.6	301	2	05QMA0_ORISA	05QMA0 cryza sativ	246	8	3.6	2414	1	EP3100_HUMAN	EP3100 human
174	8	3.6	417	2	09PUC1_BRARE	09PUC1 brachydantio	247	8	3.6	2514	2	05W1B6_HUMAN	05W1B6 homo sapien
175	8	3.6	418	2	06NV30_BRARE	06NV30 brachydantio	248	8	3.6	2539	2	04S4B6_TETNG	04S4B6 tetraodon n
176	8	3.6	418	2	06PZ26_BRARE	06PZ26 brachydantio	249	8	3.6	2730	2	04SVN3_TETNG	04SVN3 tetraodon n
177	8	3.6	419	2	050TPI_ENTHI	050TPI entamoeba h	250	8	3.6	3497	1	DMDA_DROME	DMDA drosophila

251	8	3.6	4052	2	Q70A48	ANOXA	Q79a48	anopheles	g	324	7	3.2	244	2	Q9RAE5	RHILV	Q9rae5	rhizobium	1
252	8	3.6	4061	2	Q60M30	CABER	Q60m30	caenorhabdi		325	7	3.2	247	2	Q7Z617	HUMAN	Q7z617	homo sapien	
253	8	3.6	4063	2	Q02A25	CABEL	Q02a25	caenorhabdi		326	7	3.2	251	2	Q57H24	SALCH	Q57h24	salmoneila	
254	8	3.6	4097	2	Q9VZ03	DROME	Q9vz03	drosophila		327	7	3.2	251	2	Q7CPE8	SALTY	Q7cpe8	salmoneila	
255	8	3.6	4118	2	Q7KV65	DROME	Q7kv65	drosophila		328	7	3.2	251	2	Q8XP90	SALTI	Q8xp90	salmoneila	
256	8	3.6	4207	2	Q7KV70	DROME	Q7kv70	drosophila		329	7	3.2	251	2	Q5PKV4	SALPI	Q5pkv4	salmoneila	
257	8	3.2	31	2	Q8WYF3	HUMAN	Q8wyf3	homo sapien		330	7	3.2	255	2	Q86WF6	HUMAN	Q86wf6	homo sapien	
258	7	3.2	41	2	Q9TYX5	9BIVA	Q9tyx5	mytilus. ca		331	7	3.2	266	1	PNNK1	BACSU	Q31612	bacillus su	
259	7	3.2	42	2	Q9TY10	PIAFA	Q9ty10	plasmidum		332	7	3.2	267	2	Q70Q37	GRALA	Q70q37	giardia lam	
260	7	3.2	44	2	Q9TSS4	BOVIN	Q9tss4	bos taurus		333	7	3.2	267	2	Q57652	PUGRU	Q57652	lugu rubrip	
261	7	3.2	46	2	Q3E214	9HIVI	Q3e214	human immun		334	7	3.2	268	2	Q6K2H1	ORYSA	Q6k2h1	oryza sativ	
262	7	3.2	56	2	Q7X915	WHEAT	Q7x915	tritilicum ae		335	7	3.2	269	1	MIND	GUTH	Q52316	nocardia fa	
263	7	3.2	76	2	Q5BYC6	SCHJA	Q5byc6	schistosoma		336	7	3.2	270	2	Q52316	NOCFA	Q52316	nocardia fa	
264	7	3.2	87	2	Q9FUF7	LOTPO	Q9fuf7	lotus corni		337	7	3.2	272	2	Q9LEB9	JUNGT	Q9leb9	jungius nig	
265	7	3.2	93	2	Q9SDP9	PHYCP	Q9sdp9	phytophthor		338	7	3.2	273	2	Q4V1B7	BACCC	Q4v1b7	bacillus ce	
266	7	3.2	95	2	Q5UWU0	HALMA	Q5uwu0	halotartula		339	7	3.2	278	2	Q7PUB4	ANOXA	Q7pue4	anopheles g	
267	7	3.2	102	2	Q50TW8	ENTHI	Q50tw8	entamoeba h		340	7	3.2	279	2	Q6AHQ3	CABEL	Q6ahq3	caenorhabdi	
268	7	3.2	107	2	Q5P1N6	AZOSE	Q5p1n6	azocarcus sp		341	7	3.2	291	2	Q4Q281	LEIMA	Q4q281	leishmania	
269	7	3.2	115	2	Q829B7	STRAW	Q829b7	strepcomyce		342	7	3.2	279	2	Q97FC2	CLOAB	Q97fc2	clostridium	
270	7	3.2	116	2	Q5FPT8	GLUOX	Q5fpt8	glucosinobact		343	7	3.2	282	2	Q6ACE8	9ARCH	Q6ace8	uncultured	
271	7	3.2	123	2	Q41284	GIBZE	Q41284	glibdrellia		344	7	3.2	282	2	Q5Y0M1	9ARCH	Q5y0m1	uncultured	
272	7	3.2	123	2	Q41U78	AZOVI	Q41u78	azocobacter		345	7	3.2	284	2	Q57VU1	9TRYP	Q57v1	trypanosoma	
273	7	3.2	125	2	Q14174	HOMAN	Q14174	homo sapien		346	7	3.2	290	2	Q9FWX9	ARATH	Q9fwx9	arabidopsis	
274	7	3.2	133	2	Q4ZCP3	9CAUD	Q4zcp3	bacteriophag		347	7	3.2	291	2	Q9M140	ARATH	Q9m140	arabidopsis	
275	7	3.2	133	2	Q6GAN6	STPAS	Q6gan6	staphylococc		348	7	3.2	292	2	Q8YTY9	ANASP	Q8yty9	anabaena sp	
276	7	3.2	133	2	Q6GGM1	STPAW	Q6ggm1	staphylococc		349	7	3.2	296	2	Q7Z4C7	MOUSE	Q7z4c7	mus musculu	
277	7	3.2	133	2	Q8WVH5	STPAW	Q8wvh5	staphylococc		350	7	3.2	297	2	Q74CT7	HUMAN	Q74ct7	homo sapien	
278	7	3.2	133	2	Q6DHG4	BRARE	Q6dhg4	brachydanio		351	7	3.2	300	2	Q8TLE1	METAC	Q8tle1	mechanosarc	
279	7	3.2	134	2	Q640X9	XENLA	Q640x9	xenopus lae		352	7	3.2	301	2	Q4SF76	TESTG	Q4sf76	tetradon n	
280	7	3.2	141	2	Q6ELF9	CUCSA	Q6elf9	cucumis bat		353	7	3.2	309	2	Q6ZVW9	HUMAN	Q6zv9	homo sapien	
281	7	3.2	150	2	Q70FEM4	ARALPA	Q70fem4	arabidopsis		354	7	3.2	310	2	Q50MD9	ENTHI	Q50md9	entamoeba h	
282	7	3.2	150	2	Q70FEL4	ARALPA	Q70fel4	arabidopsis		355	7	3.2	311	2	Q88016	STRCC	Q88016	strepococc	
283	7	3.2	150	2	Q70FEM1	ARALPA	Q70fem1	arabidopsis		356	7	3.2	313	2	Q8W596	MEDSA	Q8w596	medicago ba	
284	7	3.2	150	2	Q70FEM0	ARALPA	Q70fem0	arabidopsis		357	7	3.2	314	2	Q94436	9BIVA	Q94436	chlamys nlp	
285	7	3.2	152	2	Q755M6	ASHGO	Q755m6	ashbya goss		358	7	3.2	314	2	Q5ZHI9	PSEME	Q5zhi9	pseudomonas	
286	7	3.2	154	2	Q87PJ4	VIBPA	Q87pj4	vibrio para		359	7	3.2	316	2	Q85470	STRPY	Q85470	strepococc	
287	7	3.2	155	2	Q5FE209	MOUSE	Q5fe209	mus musculu		360	7	3.2	316	2	Q5XCZ9	STRPY	Q5xcz9	strepococc	
288	7	3.2	158	2	Q8CFI8	MOUSE	Q8cfi8	mus musculu		361	7	3.2	316	2	Q8K838	STRP3	Q8k838	strepococc	
289	7	3.2	162	2	Q4V739	GYIRU	Q4v739	rice tungro		362	7	3.2	319	2	Q15985	PATYB	Q15985	patinopecte	
290	7	3.2	163	2	Q7XQ51	ORYSA	Q7xq51	oryza sativ		363	7	3.2	321	2	Q15986	PATYB	Q15986	patinopecte	
291	7	3.2	172	1	LSM1	YEAST	P47017	saccharomyc		364	7	3.2	322	2	Q4FUC5	9GAMM	Q4fuc5	pychobact	
292	7	3.2	174	2	Q5JYMO	HUMAN	Q5jymo	homo sapien		365	7	3.2	324	2	Q8SP4	ORYSA	Q8sp4	oryza sativ	
293	7	3.2	174	2	Q4UGV8	THEAN	Q4ugv8	theileria a		366	7	3.2	325	2	Q09344	PATYB	Q09344	patinopecte	
294	7	3.2	175	2	Q6GGM6	GYIRU	Q6ggm6	infectious		367	7	3.2	327	2	Q75FZ9	LEPIC	Q75fz9	leptospira	
295	7	3.2	175	2	Q6GGM7	GYIRU	Q6ggm7	infectious		368	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
296	7	3.2	175	2	Q6GGM8	GYIRU	Q6ggm8	infectious		369	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
297	7	3.2	175	2	Q6GGM9	GYIRU	Q6ggm9	infectious		370	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
298	7	3.2	175	2	Q6GGM9	GYIRU	Q6ggm9	infectious		371	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
299	7	3.2	175	2	Q6GGM9	GYIRU	Q6ggm9	infectious		372	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
300	7	3.2	175	2	Q6GGM9	GYIRU	Q6ggm9	infectious		373	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
301	7	3.2	175	2	Q6GGM9	GYIRU	Q6ggm9	infectious		374	7	3.2	327	2	Q8EYJ9	LEPIN	Q8eyj9	leptospira	
302	7	3.2	179	2	Q6XMX0	HUMAN	Q6xmx0	homo sapien		375	7	3.2	340	2	Q8GSM4	ARATH	Q8gsm4	arabidopsis	
303	7	3.2	182	2	Q5QXK6	IDILO	Q5qxk6	idionaria		376	7	3.2	340	2	Q8GSM4	ARATH	Q8gsm4	arabidopsis	
304	7	3.2	184	2	Q9TUP8	PIG	Q9tup8	sus scrofa		377	7	3.2	340	2	Q8GRV6	ARATH	Q8grv6	arabidopsis	
305	7	3.2	185	2	Q7NMS9	GLOVI	Q7nms9	gloeobacter		378	7	3.2	340	2	Q8GS44	ARATH	Q8gs44	arabidopsis	
306	7	3.2	186	2	Q8W220	HUMAN	Q8w220	homo sapien		379	7	3.2	341	1	TRPD	BACCR	Q8w220	homo sapien	
307	7	3.2	186	2	Q810R2	MOUSE	Q810r2	mus musculu		380	7	3.2	341	2	Q7XAN0	ORYSA	Q7xan0	oryza sativ	
308	7	3.2	191	2	Q84S95	RAPSA	Q84s95	raphanus ma		381	7	3.2	342	2	Q6DH60	BRARE	Q6dh60	brachydanio	
309	7	3.2	211	2	Q4P4V2	USTMA	Q4p4v2	ustilago ma		382	7	3.2	343	2	Q4HZE2	GIBZE	Q4hze2	gibberella	
310	7	3.2	213	2	Q8EMG7	OCEIH	Q8emg7	oceanobact		383	7	3.2	343	2	Q9S035	BORBU	Q9s035	borrelia bu	
311	7	3.2	215	2	Q8TCN6	HUMAN	Q8tcn6	homo sapien		384	7	3.2	344	2	Q9W3J7	DROME	Q9w3j7	drosophila	
312	7	3.2	215	2	Q5SQS6	HUMAN	Q5sq66	homo sapien		385	7	3.2	344	2	Q9AKB7	ARALP	Q9akb7	arabidopsis	
313	7	3.2	217	2	Q7Z2X0	HUMAN	Q7z2x0	homo sapien		386	7	3.2	344	2	Q4IVX3	AZOVI	Q4ivx3	azotobacter	
314	7	3.2	218	2	Q9HSM4	HALSA	Q9hsm4	halobacteri		387	7	3.2	344	2	Q92Q29	RHIME	Q92q29	rhizobium m	
315	7	3.2	224	2	Q7NMO8	CHARVO	Q7nmo8	chromobact		388	7	3.2	345	2	Q5ZNO6	PSEOL	Q5zno6	pseudomonas	
316	7	3.2	231	2	Q5BWK9	SACOF	Q5bwk9	saccharum o		389	7	3.2	346	2	Q9DAC6	MOUSE	Q9dac6	mus musculu	
317	7	3.2	231	2	Q5OLU4	ORYSA	Q5olu4	oryza sativ		390	7	3.2	346	2	Q569C2	NAT	Q569c2	natu nov	
318	7	3.2	233	2	Q826B5	STRAW	Q826b5	strepococc		391	7	3.2	347	2	Q160B1	HUMAN	Q160b1	homo sapien	
319	7	3.2	233	2	Q729K9	DESIVH	Q729k9	mycoplasma		392	7	3.2	347	2	Q82VX4	NITRU	Q82vx4	nitrososoma	
320	7	3.2	237	1	GIDB	MYCPE	Q8euv9	mycoplasma		393	7	3.2	348	2	Q6ZWR1	MOUSE	Q6zwr1	mus musculu	
321	7	3.2	237	1	Q6G5R3	BARHE	Q6g5r3	bartheletia		394	7	3.2	350	2	Q6AHQ2	CABEL	Q6ahq2	caenorhabdi	
322	7	3.2	237	2	Q97TUD	CLOAB	Q97tuo	clostridium		395	7	3.2	354	2	Q51EW3	ENTHI	Q51ew3	entamoeba h	
323	7	3.2	244	2	P72285	RHILE	P72285	rhizobium 1		396	7	3.2	355	2	Q4QURE	APICR	Q4qur8	apium grave	

397	7	3.2	356	1	FL3H_CALCH	Q05963	callistephu
398	7	3.2	357	1	FL3H_MATIN	Q05965	matchiola l
399	7	3.2	357	2	Q6VZ3_HUMAN	Q6vz3	homo sapien
400	7	3.2	357	2	Q5SQS_HUMAN	Q5sqgs	homo sapien
401	7	3.2	357	2	Q49982_9ASTR	Q49982	chrysanthem
402	7	3.2	357	2	Q40344_MEDSA	Q40344	medicago sa
403	7	3.2	357	2	Q42927_MEDSA	Q42927	medicago sa
404	7	3.2	357	2	Q4QUR9_DAVCA	Q4qur9	daucus caro
405	7	3.2	357	2	Q9X221_THEMA	Q9x221	thermopoga
406	7	3.2	358	1	FL3H_ARATH	Q9x818	arabidopsis
407	7	3.2	358	1	Q56180_9GOLN	Q56180	solanum pin
408	7	3.2	358	2	Q5DWM0_ARATH	Q5dwm0	arabidopsis
409	7	3.2	358	2	Q818C8_SOLITU	Q818c8	solanum tub
410	7	3.2	359	2	Q68G19_9BACT	Q68g19	uncultured
411	7	3.2	359	2	Q6UCT3_9GAMM	Q6uct3	uncultured
412	7	3.2	361	2	Q7SZ61_BRARE	Q7sz61	brachydanio
413	7	3.2	362	2	Q9ZMR0_CITST	Q9zmr0	citrus sine
414	7	3.2	363	2	Q6BEH2_EUSGR	Q6beh2	eubetoma gra
415	7	3.2	364	1	FL3H_VITVI	P41090	vitis vinif
416	7	3.2	364	2	Q66ME9_FRAN	Q66me9	fragaria an
417	7	3.2	364	2	Q66MFO_FRAN	Q66mfo	fragaria an
418	7	3.2	365	2	Q59170_GENTR	Q59170	gentiana tr
419	7	3.2	365	2	Q59170_GENTR	Q59170	gentiana tr
420	7	3.2	365	2	Q7XZQ8_PETCR	Q7xzq8	petroselinu
421	7	3.2	365	2	Q4QUS0_9APIA	Q4qus0	pimpinella
422	7	3.2	365	2	Q7NOL3_CHRYO	Q7nol3	chromobacte
423	7	3.2	365	2	Q23825_IIRONI	Q23825	ipomoea nil
424	7	3.2	366	2	Q23825_IIRONI	Q23825	ipomoea nil
425	7	3.2	366	2	Q9SP53_DAVCA	Q9sp53	daucus caro
426	7	3.2	366	2	Q4QUR5_9APIA	Q4qur5	anethum gra
427	7	3.2	367	2	Q8LP21_9SOLA	Q8lp21	niemembergi
428	7	3.2	367	2	Q96472_IPOPU	Q96472	ipomoea pur
429	7	3.2	368	2	Q6DV45_CAMSI	Q6dv45	camellia si
430	7	3.2	368	2	Q7XZQ7_PETCR	Q7xzq7	petroselinu
431	7	3.2	368	2	Q9SX85_IPOBA	Q9sx85	ipomoea bat
432	7	3.2	368	2	Q9ZQ57_IPOBA	Q9zq57	ipomoea bat
433	7	3.2	368	2	Q9ZQ58_IPOBA	Q9zq58	ipomoea bat
434	7	3.2	368	2	Q4QUR6_9APIA	Q4qur6	ammi majus
435	7	3.2	370	2	Q5ZH06_PSRPS	Q5zh06	homo sapien
436	7	3.2	370	2	Q5ZH06_PSRPS	Q5zh06	pseudomonas
437	7	3.2	372	2	Q6EP43_9LAMI	Q6ep43	sinningia c
438	7	3.2	376	1	MJD1_HUMAN	P54252	homo sapien
439	7	3.2	380	2	Q9AS74_ORYSA	Q9as74	oryza sativ
440	7	3.2	381	2	Q5ZN27_PSEME	Q5zn27	pseudomonas
441	7	3.2	382	2	Q5ZH39_PSEME	Q5zh39	pseudomonas
442	7	3.2	384	2	Q5ZN37_PSRPS	Q5zn37	pseudomonas
443	7	3.2	386	2	Q54UN5_DICDI	Q54un5	dicyostelei
444	7	3.2	387	2	Q5ZH46_PSRPS	Q5zh46	pseudomonas
445	7	3.2	393	2	Q50W31_ENTHI	Q50w31	entamoeba h
446	7	3.2	395	2	Q5AV11_EMENTI	Q5av11	aspergillus
447	7	3.2	396	2	Q537T8_NBIEM	Q537t8	neisseria m
448	7	3.2	397	2	Q92D08_LISIN	Q92d08	listeria in
449	7	3.2	397	2	Q721P2_LISIN	Q721f2	listeria mo
449	7	3.2	397	2	Q721P2_LISIN	Q721f2	listeria mo
450	7	3.2	397	2	Q9RR46_LISMO	Q9rr46	listeria mo
451	7	3.2	400	1	Q6C4S1_YARLI	Q6c4s1	yarrowia li
452	7	3.2	401	1	COAT_PAV	Q91720	paratocov v
453	7	3.2	402	2	Q75LZ5_ORYSA	Q75l25	oryza sativ
454	7	3.2	403	2	Q4K7X1_PSRPS	Q4k7x1	pseudomonas
455	7	3.2	406	2	Q4R0B6_TETNG	Q4rueb	tetradon n
456	7	3.2	408	1	PGK_SUTSO	P50317	sulfolobus
457	7	3.2	410	2	Q71SA7_ORYSA	Q71sa7	oryza sativ
458	7	3.2	410	2	Q53NF8_ORYSA	Q53nf8	oryza sativ
459	7	3.2	411	2	Q13108_BRARE	Q13108	brachydanio
460	7	3.2	411	2	Q57573_BRARE	Q57573	brachydanio
461	7	3.2	411	2	Q93369_BRARE	Q93369	brachydanio
462	7	3.2	412	1	APK1B_ARATH	P46573	arabidopsis
463	7	3.2	413	1	Q7GAG3_ARATH	Q7gag3	arabidopsis
464	7	3.2	413	1	RFIM_YEAST	P30775	saccharomyc
465	7	3.2	415	2	Q6RTJ1_CANGA	Q6rfj1	candida gla
466	7	3.2	415	2	Q7XAM9_ORYSA	Q7xam9	oryza sativ
467	7	3.2	416	2	Q7S116_NEUCR	Q7s116	neurospora
468	7	3.2	419	2	Q5B969_EMENTI	Q5b969	aspergillus
469	7	3.2	419	2	Q7VFD4_HELHP	Q7vfd4	helicobacte
470	7	3.2	419	2	Q6UD79_ONCMY	Q6ud79	oncorhynch
471	7	3.2	422	2	Q4WVZ8_ASPFU	Q4wvz8	aspergillus
472	7	3.2	423	2	Q8ROA3_MOUSE	Q8roa3	mus musculus
473	7	3.2	423	2	Q7SZM3_ICTPU	Q7szm3	ictalurus p
474	7	3.2	423	2	Q60U36_CABER	Q60u36	canorhabdi
475	7	3.2	428	2	Q808D4_VYIRU	Q808d4	nummichog a
476	7	3.2	428	2	Q808D5_VYIRU	Q808d5	flounder aq
477	7	3.2	431	2	Q5S0S7_HUMAN	Q5s0s7	homo sapien
478	7	3.2	433	2	Q22093_CAEEL	Q22093	caenorhabdi
479	7	3.2	442	2	Q80B00_VYIRU	Q80b00	infectious
480	7	3.2	450	2	Q65106_BACLD	Q65106	bacillus li
481	7	3.2	451	2	Q4T9X0_TETNG	Q4t9x0	tetradon n
482	7	3.2	453	2	Q5M17_CRYNE	Q5m17	cryptococcu
483	7	3.2	453	2	Q5KX77_CRYNE	Q5kx77	cryptococcu
484	7	3.2	455	2	Q9GTW7_DROYA	Q9gtw7	drosophila
485	7	3.2	460	2	Q51F81_ENTHI	Q51fb1	entamoeba h
486	7	3.2	465	2	Q51U30_MAGGR	Q51u30	magnaporthe
487	7	3.2	468	2	Q9H6A0_HUMAN	Q9h6a0	homo sapien
488	7	3.2	468	2	Q5TV6_HUMAN	Q5tv6	homo sapien
489	7	3.2	470	2	Q9T0C4_ARATH	Q9t0c4	arabidopsis
490	7	3.2	471	2	Q9BSU0_HUMAN	Q9bsu0	homo sapien
491	7	3.2	472	2	Q5CZV9_BRARE	Q5czv9	brachydanio
492	7	3.2	476	2	Q4YT37_PLABE	Q4yt37	plasmidum
493	7	3.2	478	2	Q97TX5_SUTSO	Q97tx5	sulfolobus
494	7	3.2	481	2	Q54072_SACER	Q54072	saccharopol
495	7	3.2	483	2	Q62WQ0_MOUSE	Q62wq0	mus musculus
496	7	3.2	483	2	Q61WL3_BRARE	Q61wl3	brachydanio
497	7	3.2	488	2	Q50LW0_ENTHI	Q50lw0	entamoeba h
498	7	3.2	496	2	Q4MLM8_BACCE	Q4mlm8	bacillus ce
499	7	3.2	498	2	Q56776_XANCA	Q56776	xanthomonas
500	7	3.2	498	2	Q9QSU8_9ITVI	Q9qsu8	human timun
501	7	3.2	499	2	Q4UM41_XANCP	Q4um41	xanthomonas
502	7	3.2	499	2	Q8P805_XANCP	Q8p805	xanthomonas
503	7	3.2	500	2	Q5A2J1_CANAL	Q5a2j1	candida alb
504	7	3.2	501	2	Q8DUU0_STRMU	Q8duu0	streptococc
505	7	3.2	502	2	Q4RVA3_TETNG	Q4rv43	tetradon n
506	7	3.2	505	2	Q6EDU0_HUMAN	Q6edu0	homo sapien
507	7	3.2	507	2	Q670Q4_EMENTI	Q670q4	emeritella
508	7	3.2	507	2	Q5KKN8_CRYNE	Q5kkn8	cryptococcu
509	7	3.2	507	2	Q5SVK0_CRYNE	Q5svk0	cryptococcu
510	7	3.2	508	2	Q5BK99_DBBNA	Q5bk99	debrayomyce
511	7	3.2	508	2	Q5LJRE_MAGCR	Q5ljre	magnaporthe
512	7	3.2	510	2	Q4VM06_9ROSI	Q4vm06	securinega
513	7	3.2	510	2	Q63ZU0_MOUSE	Q63zu0	mus musculus
514	7	3.2	515	1	C13A2_CABSL	Q27518	caenorhabdi
515	7	3.2	515	1	Q4WY05_ASPFU	Q4wy05	aspergillus
516	7	3.2	515	2	Q4RBB7_MOUSE	Q4rbh7	mus musculus
517	7	3.2	520	2	Q21020_CABEL	Q21020	canorhabdi
518	7	3.2	523	2	Q8AV90_PETMA	Q8av90	petromyzon
519	7	3.2	528	2	Q6ZWN0_MOUSE	Q6zwn0	mus musculus
520	7	3.2	529	2	Q55SL4_CRYNE	Q55sl4	cryptococcu
521	7	3.2	529	2	Q5KH05_CRYNE	Q5kh05	cryptococcu
522	7	3.2	530	2	Q5BAZ9_CRYNE	Q5baz9	aspergillus
523	7	3.2	534	2	Q9HA36_HUMAN	Q9ha36	homo sapien
524	7	3.2	538	1	GLE1_YEAST	Q12135	bacharomyc
525	7	3.2	539	2	Q7S7G8_NEUCR	Q7s7g8	neurospora
526	7	3.2	539	2	Q8BBY0_MOUSE	Q8bb0	mus musculus
527	7	3.2	540	2	Q6ALB3_DEESP	Q6alb3	desulfotale
528	7	3.2	543	2	Q93S09_STRCO	Q93s09	strepomyce
529	7	3.2	544	2	Q6PE01_MOUSE	Q6pe01	mus musculus
530	7	3.2	545	2	Q9HEK1_NEUCR	Q9hek1	neurospora
531	7	3.2	547	2	Q4MYE8_TBRPA	Q4mye8	thelateria p
532	7	3.2	547	2	Q4Q8N0_LEIMA	Q4q8n0	leishmania
533	7	3.2	548	1	GNL3_XENTR	Q6p475	xenopus tro
534	7	3.2	548	2	Q9RW08_DEIRA	Q9rw08	delinococcus
535	7	3.2	549	2	Q64B31_9ARCH	Q64b31	uncultured
536	7	3.2	549	2	Q8NA37_HUMAN	Q8na37	homo sapien
537	7	3.2	549	2	Q74F53_GEOSL	Q74f53	geobacter s
538	7	3.2	552	2	Q6A077_MOUSE	Q6a077	mus musculus
539	7	3.2	555	2	Q81VP9_HUMAN	Q81vf9	homo sapien
540	7	3.2	555	2	Q9U0V4_LEIMA	Q9u0v4	leishmania
541	7	3.2	557	2	Q4UB78_THEAN	Q4ub78	thelateria a
542	7	3.2	560	2	Q4NUZ0_9DELT	Q4nuz0	anaeromyxob

543	7	3.2	561	2	Q4WLR7_ASPFU	Q4WLR7 aspergillus	616	7	3.2	730	2	Q7XLR2_ORYSA	Q7XLR2 oryza sativ
544	7	3.2	564	2	Q5BCK1_EMENTI	Q5BCK1 aspergillus	617	7	3.2	733	2	Q5LQ74_MAGGR	Q5LQ74 magnaporthe
545	7	3.2	566	2	Q7RW0_NEUCR	Q7RW0 neurospora	618	7	3.2	737	2	Q5BR1_EMENTI	Q5BR1 aspergillus
546	7	3.2	565	2	Q60TR6_CABBR	Q60TR6 caenorhabdi	619	7	3.2	738	2	Q5OTC4_ENTHI	Q5OTC4 entamoeba h
547	7	3.2	568	2	Q6NVM1_XENTR	Q6NVM1 xenopus tro	620	7	3.2	739	2	Q6SD8_ORYSA	Q6SD8 oryza sativ
548	7	3.2	574	2	Q5ZJ72_CHICK	Q5ZJ72 gallus gall	621	7	3.2	741	2	Q6LN22_CABBR	Q6LN22 caenorhabdi
549	7	3.2	579	2	Q7TNZ7_RAT	Q7TNZ7 rattus norv	622	7	3.2	743	2	Q6ZN50_HUMAN	Q6ZN50 homo sapien
550	7	3.2	580	2	Q4FEZ1_RAT	Q4FEZ1 rattus norv	623	7	3.2	755	2	Q9X180_THEMA	Q9X180 thermoga
551	7	3.2	581	2	Q8BX57_MOUSE	Q8BX57 mus musculu	624	7	3.2	768	2	Q8C585_MOUSE	Q8C585 mus musculu
552	7	3.2	582	2	Q91WB6_MOUSE	Q91WB6 mus musculu	625	7	3.2	771	2	Q8RUB5_METMA	Q8RUB5 methanobarc
553	7	3.2	593	2	Q4QR28_LEIMA	Q4QR28 leishmania	626	7	3.2	771	2	Q7PXB1_ANOGA	Q7PXB1 anopheles g
554	7	3.2	594	2	Q81129_CABEL	Q81129 caenorhabdi	627	7	3.2	784	1	GBR_PLAFG	P02895 plasmodium
555	7	3.2	595	2	KINB_PSEAE	Q34206 pseudomonas	628	7	3.2	785	2	Q7D3D9_AGR75	Q7D3D9 agrobacteri
556	7	3.2	595	2	Q9HT87_PSEAE	Q9HT87 pseudomonas	629	7	3.2	789	2	Q5R6N7_PONPY	Q5R6N7 pongo pygma
557	7	3.2	597	2	Q4WV4_ASPFU	Q4WV4 aspergillus	630	7	3.2	798	2	Q5BR22_EMENTI	Q5BR22 aspergillus
558	7	3.2	597	2	Q7U2T5_MYCBO	Q7U2T5 mycobacteri	631	7	3.2	798	2	Q9NVA7_HUMAN	Q9NVA7 homo sapien
559	7	3.2	600	2	Q4J3V8_AZOV1	Q4J3V8 azotobacter	632	7	3.2	799	2	Q7Z3K9_HUMAN	Q7Z3K9 homo sapien
560	7	3.2	602	2	Q9P8C3_9HPYO	Q9P8C3 acetonitum	633	7	3.2	799	2	Q8V3M3_SWPV	Q8V3M3 swinepox vi
561	7	3.2	603	2	Q9NMW6_HUMAN	Q9NMW6 homo sapien	634	7	3.2	801	2	Q6PIZ0_HUMAN	Q6PIZ0 homo sapien
562	7	3.2	606	2	Q9Z2J3_RAT	Q9Z2J3 rattus norv	635	7	3.2	804	2	Q8V3M3_SWPV	Q8V3M3 swinepox vi
563	7	3.2	607	2	Q7TPW1_MOUSE	Q7TPW1 mus musculu	636	7	3.2	805	2	Q5EBM3_HUMAN	Q5EBM3 homo sapien
564	7	3.2	610	2	Q4HZK8_GIBZE	Q4HZK8 gibberella	637	7	3.2	807	2	Q7TIB6_FUGRU	Q7TIB6 fugu rubrip
565	7	3.2	612	2	Q7X678_CHLRE	Q7X678 chlamydomon	638	7	3.2	807	2	Q8AXT1_FUGRU	Q8AXT1 xyella fas
566	7	3.2	614	2	Q55YK6_CRYNE	Q55YK6 cryptococcu	639	7	3.2	809	1	PBPX_XYLPA	Q8C9G1 xyella fas
567	7	3.2	614	2	Q5XLD2_CRYNE	Q5XLD2 cryptococcu	640	7	3.2	809	1	PBPX_XYLPA	Q8C9G1 xyella fas
568	7	3.2	615	2	Q6ZWR5_MOUSE	Q6ZWR5 mus musculu	641	7	3.2	809	2	Q8CGG1_MOUSE	Q8CGG1 mus musculu
569	7	3.2	619	2	Q6KKX0_HUMAN	Q6KKX0 homo sapien	642	7	3.2	809	2	Q6PAR2_MOUSE	Q6PAR2 mus musculu
570	7	3.2	621	2	Q5BDB4_EMENTI	Q5BDB4 aspergillus	643	7	3.2	812	2	Q7R1L8_GIALA	Q7R1L8 giardia lam
571	7	3.2	621	2	Q4WQLE_ASPFU	Q4WQLE aspergillus	644	7	3.2	816	2	Q5ZL41_CHICK	Q5ZL41 gallus gall
572	7	3.2	621	2	Q49047_TOBAC	Q49047 nicotiana t	645	7	3.2	819	2	Q8UK13_AGR75	Q8UK13 agrobacteri
573	7	3.2	624	1	PARN_MOUSE	Q8V6G3 mus musculu	646	7	3.2	822	2	Q91288_PLEMA	Q91288 pleurodeles
574	7	3.2	630	2	Q5P670_AZOSE	Q5P670 azaracus sp	647	7	3.2	824	1	GBR_PLAF7	Q816U8 plasmodium
575	7	3.2	633	1	P6GA_HUMAN	Q86P4 homo sapien	648	7	3.2	828	1	SKOR_ARATH	Q816U8 plasmodium
576	7	3.2	633	2	Q98LR9_RHIL0	Q98LR9 rhizobium l	649	7	3.2	831	2	Q7S5Z4_NEUCR	Q7S5Z4 neurospora
577	7	3.2	633	2	Q926H1_RHIME	Q926H1 rhizobium m	650	7	3.2	842	2	Q54MH2_DICDI	Q54MH2 dictyosteli
578	7	3.2	637	1	SYT_CHILAB	Q514C1 chlamydomon	651	7	3.2	843	2	Q6AXC9_MOUSE	Q6AXC9 mus musculu
579	7	3.2	637	1	Q5DZP9_VIBF1	Q5DZP9 vibrio flic	652	7	3.2	849	2	Q5R68_DROME	Q5R68 drosophila
580	7	3.2	639	1	PARN_HUMAN	Q95453 homo sapien	653	7	3.2	856	2	Q8B1P8_ARATH	Q8B1P8 arabidopsi
581	7	3.2	639	1	PARN_PONPY	Q5R551 pongo pygma	654	7	3.2	857	1	GELA_DICDI	Q816U8 plasmodium
582	7	3.2	651	2	Q6EPU8_BRARE	Q6EPU8 brachydanio	655	7	3.2	857	1	Q5C12_DICDI	Q5C12 dictyosteli
583	7	3.2	656	1	R1PK1_MOUSE	Q60855 mus musculu	656	7	3.2	861	2	Q6VLX2_DROME	Q6VLX2 drosophila
584	7	3.2	656	1	Q9Z2J4_RAT	Q9Z2J4 rattus norv	657	7	3.2	871	2	Q8VP66_THIEYO	Q8VP66 thermoe
585	7	3.2	669	2	Q4JOE8_AZOV1	Q4JOE8 azotobacter	658	7	3.2	871	2	Q8RBE6_THIEN	Q8RBE6 thermoe
586	7	3.2	669	2	Q88CB7_PSEPK	Q88CB7 pseudomonas	659	7	3.2	875	2	Q5Y2P9_DBRPT	Q5Y2P9 dermatophag
587	7	3.2	669	2	Q9HTO8_PSEAE	Q9HTO8 pseudomonas	660	7	3.2	876	1	MISP_SARSC	Q9HMM8 sarcopetes s
588	7	3.2	676	2	Q84Q65_ORYSA	Q84Q65 oryza sativ	661	7	3.2	876	2	Q17951_CABEL	Q17951 caenorhabdi
589	7	3.2	687	2	Q5P6M5_AZOSE	Q5P6M5 azaracus sp	662	7	3.2	876	2	Q7TN28_MOUSE	Q7TN28 mus musculu
590	7	3.2	688	1	DNLJ_THEMA	Q9W4V5 thermoe	663	7	3.2	877	1	INCE_CHICK	P53352 gallus gall
591	7	3.2	690	1	EPB42_HUMAN	P16452 homo sapien	664	7	3.2	878	1	Q5BP2_HUMAN	Q5BP2 homo sapien
592	7	3.2	691	2	Q4YB97_HUMAN	Q4YB97 homo sapien	665	7	3.2	878	2	Q5AS58_EMENTI	Q5AS58 aspergillus
593	7	3.2	692	1	MISP_DBRPA	Q96720 dermatophag	666	7	3.2	880	1	INCE_MOUSE	Q5A662 mus musculu
594	7	3.2	692	1	Q7SE14_NEUCR	Q7SE14 neurospora	667	7	3.2	880	2	Q8PGY9_XANAC	Q8PGY9 xanthomonas
595	7	3.2	695	2	Q521Y5_MAGGR	Q521Y5 magnaporthe	668	7	3.2	881	2	Q5H3V2_XANOR	Q5H3V2 xanthomonas
596	7	3.2	695	2	Q7ZUM8_BRARE	Q7ZUM8 brachydanio	669	7	3.2	886	2	Q9VZ04_DROME	Q9VZ04 drosophila
597	7	3.2	698	2	Q8NC60_HUMAN	Q8NC60 homo sapien	670	7	3.2	892	2	Q4SC70_THIEN	Q4SC70 thermoe
598	7	3.2	698	2	Q8BSQ8_HUMAN	Q8BSQ8 homo sapien	671	7	3.2	899	2	Q7QEZ3_ANOGA	Q7QEZ3 anopheles g
599	7	3.2	700	1	SYNG_RAT	Q9JYK9 rattus norv	672	7	3.2	908	2	Q5QON6_MOUSE	Q5QON6 mus musculu
600	7	3.2	701	2	Q4K3R2_PSEPF	Q4K3R2 pseudomonas	673	7	3.2	914	2	Q5THY6_HUMAN	Q5THY6 entamoeba h
601	7	3.2	701	2	Q9HTMO_PSEAE	Q9HTMO pseudomonas	674	7	3.2	917	2	Q5THY6_HUMAN	Q5THY6 entamoeba h
602	7	3.2	702	2	Q88BE4_PSEPM	Q88BE4 pseudomonas	675	7	3.2	918	2	Q5Y192_HUMAN	Q5Y192 homo sapien
603	7	3.2	702	2	Q88CB1_PSEPK	Q88CB1 pseudomonas	676	7	3.2	919	1	INCE_HUMAN	Q5Y192 homo sapien
604	7	3.2	704	2	Q4P665_USTMA	Q4P665 usellago ma	677	7	3.2	922	2	Q8RFX5_ARATH	Q8RFX5 arabidopsi
605	7	3.2	705	2	Q82496_ARATH	Q82496 arabidopsi	678	7	3.2	923	2	Q6U424_HUMAN	Q6U424 homo sapien
606	7	3.2	707	2	Q4Z2Z0_PESBY	Q4Z2Z0 pseudomonas	679	7	3.2	937	2	Q7ZUV4_BRARE	Q7ZUV4 brachydanio
607	7	3.2	708	2	Q873AO_NEUCR	Q873AO neurospora	680	7	3.2	940	2	Q6CAR0_YARLI	Q6CAR0 yarrowia li
608	7	3.2	712	2	Q4K686_PSEFS	Q4K686 pseudomonas	681	7	3.2	945	2	Q7P6J0_FUSNV	Q7P6J0 fusobacteri
609	7	3.2	714	1	BEGL_MYCTU	Q07170 mycobacteri	682	7	3.2	948	2	Q6BKT9_DBRHA	Q6BKT9 debaryomyce
610	7	3.2	718	2	OSIUL4_MAGGR	OSIUL4 magnaporthe	683	7	3.2	955	2	Q75DB7_ASHGO	Q75DB7 ashbya gos
611	7	3.2	718	2	Q9NVQ0_HUMAN	Q9NVQ0 homo sapien	684	7	3.2	960	2	Q8L671_ORYSA	Q8L671 oryza sativ
612	7	3.2	720	2	Q7JU43_MYCPA	Q7JU43 mycobacteri	685	7	3.2	964	2	Q42489_CHICK	Q42489 gallus gall
613	7	3.2	728	2	Q7SELO_NEUCR	Q7SELO neurospora	686	7	3.2	967	2	Q84FK8_ENTAG	Q84FK8 enterobacte
614	7	3.2	728	2	Q7ZJ86_THET2	Q7ZJ86 thermus the	687	7	3.2	968	2	Q990M5_VIVIRU	Q990M5 infectio
615	7	3.2	728	2	Q561V7_THET8	Q561V7 thermus the	688	7	3.2	968	2	Q990M6_VIVIRU	Q990M6 infectio

689	7	3.2	968	2	Q990M7	9VIRU	Q990m7	infectious	762	7	3.2	1254	2	Q29122	PIG	Q29122	bus	acrofa
690	7	3.2	968	2	Q990M8	9VIRU	Q990m8	infectious	763	7	3.2	1255	2	Q6B335	BRARE	Q6B335	brachydantio	
691	7	3.2	968	2	Q990P3	9VIRU	Q990p3	infectious	764	7	3.2	1256	2	Q4WJW2	ASPFU	Q4WJW2	aspergillus	
692	7	3.2	968	2	Q990Q1	9VIRU	Q990q1	infectious	765	7	3.2	1257	1	FLII	CABEL	P34268	caenorhabd1	
693	7	3.2	970	2	Q4TLU5	95PHN	Q4tlus	elythrobact	766	7	3.2	1262	2	OSTEM7	HUMAN	OSTEM7	homo sapien	
694	7	3.2	972	1	POLS	IPNVJ	P05844	infectious	767	7	3.2	1265	1	MYO6	MOUSE	Q64331	mus musculu	
695	7	3.2	972	2	Q7TLC2	9VIRU	Q7tlc2	infectious	768	7	3.2	1267	2	Q9N8F0	STRPU	Q9n8f0	strongyloce	
696	7	3.2	972	2	Q827J3	9VIRU	Q827j3	infectious	769	7	3.2	1267	2	Q68R03	BRARS	Q68r03	brachydantio	
697	7	3.2	972	2	Q8JTK5	9VIRU	Q8jtk5	infectious	770	7	3.2	1268	2	Q7RG05	PLAYO	Q7rg05	plasmodium	
698	7	3.2	972	2	Q9WLE3	9VIRU	Q9wle3	infectious	771	7	3.2	1276	2	Q91BD1	CHICK	Q91bd1	gallus gall	
699	7	3.2	972	2	Q6OE16	ORYSA	Q6oe16	oryza sativ	772	7	3.2	1285	1	MYO6	HUMAN	MYO6	homo sapien	
700	7	3.2	980	2	Q5U7X8	9VIRU	Q5u7x8	infectious	773	7	3.2	1291	2	Q6Y7W8	MOUSE	Q6y7w8	mus musculu	
701	7	3.2	980	2	Q5U7Y0	9VIRU	Q5u7y0	infectious	774	7	3.2	1291	2	Q68R02	BRARS	Q68r02	brachydantio	
702	7	3.2	980	2	Q5U7Y4	9VIRU	Q5u7y4	infectious	775	7	3.2	1292	2	Q723J2	HUMAN	Q723j2	homo sapien	
703	7	3.2	980	2	Q5U7Y6	9VIRU	Q5u7y6	infectious	776	7	3.2	1298	2	Q6Y7W6	HUMAN	Q6y7w6	homo sapien	
704	7	3.2	980	2	Q5U7Z0	9VIRU	Q5u7z0	infectious	777	7	3.2	1299	2	Q722Z8	HUMAN	Q722z8	homo sapien	
705	7	3.2	982	2	Q4KZV0	TECTNG	Q4kzv0	tetradodon n	778	7	3.2	1299	2	Q6GLR7	XENILA	Q6glr7	xenopus lae	
706	7	3.2	990	2	Q56YV1	ARATH	Q56yvp1	arabidopsis	779	7	3.2	1299	2	Q6GLR7	XENILA	Q6glr7	xenopus lae	
707	7	3.2	991	2	Q56YV2	ARATH	Q56ym2	arabidopsis	780	7	3.2	1306	1	SYNG	HUMAN	SYNG	homo sapien	
708	7	3.2	991	2	Q56YV0	ARATH	Q56yr0	arabidopsis	781	7	3.2	1314	1	Q9UPF8	HUMAN	Q9upf8	homo sapien	
709	7	3.2	991	2	Q56YV4	ENTHI	Q56y4	entamoeba h	782	7	3.2	1315	2	Q75137	HUMAN	Q75137	homo sapien	
710	7	3.2	997	2	Q54YB5	DICDI	Q54yb5	dictyosteli	783	7	3.2	1329	2	Q4KME6	BRARE	Q4kme6	brachydantio	
711	7	3.2	1002	1	CLNM	HUMAN	Q54yb5	dictyosteli	784	7	3.2	1335	1	SRC3	YEAST	SRC3	saccharomyc	
712	7	3.2	1002	2	Q6NUQ2	HUMAN	Q6nuq2	homo sapien	785	7	3.2	1336	2	Q6N8E5	NEUCR	Q6n8e5	neurospora	
713	7	3.2	1018	2	Q753P3	ASHGO	Q753p3	ashbya gos	786	7	3.2	1367	2	Q4LB49	HUMAN	Q4lb49	homo sapien	
714	7	3.2	1018	2	Q5V568	ORYSA	Q5v568	oryza sativ	787	7	3.2	1374	2	Q815S6	PLAF7	Q815s6	plasmidium	
715	7	3.2	1028	2	Q5VU16	HUMAN	Q5v16	homo sapien	788	7	3.2	1377	2	Q815S6	PLAF7	Q815s6	plasmidium	
716	7	3.2	1028	2	Q04604	ARATH	Q04604	arabidopsis	789	7	3.2	1407	1	Q4T3R1	TECTNG	Q4t3r1	tetradodon n	
717	7	3.2	1032	2	Q4XVW2	PLACH	Q4xvw2	plasmodium	790	7	3.2	1414	2	Q4T3R1	TECTNG	Q4t3r1	tetradodon n	
718	7	3.2	1032	2	Q6QM03	AEGETA	Q6qm03	aegilops ta	791	7	3.2	1418	2	Q8K3V7	MOUSE	Q8k3v7	mus musculu	
719	7	3.2	1036	2	Q4WYU6	ASPFU	Q4wyu6	aspergillus	792	7	3.2	1426	2	Q8K3V7	MOUSE	Q8k3v7	mus musculu	
720	7	3.2	1042	2	Q4Q5S2	LEIMA	Q4q5s2	leishmania	793	7	3.2	1431	2	Q4N018	THEPA	Q4n018	thelema p	
721	7	3.2	1045	2	Q6NKKY	DROME	Q6nkk5	drosophila	794	7	3.2	1440	2	Q4YZ38	PLABE	Q4yz38	plasmidium	
722	7	3.2	1046	2	Q6NN85	DROME	Q6nn85	drosophila	795	7	3.2	1448	2	Q53NR4	ORYSA	Q53nr4	oryza sativ	
723	7	3.2	1048	2	Q80TV1	MOUSE	Q80tv1	mus musculu	796	7	3.2	1497	2	Q4WC64	ASPFU	Q4wc64	aspergillus	
724	7	3.2	1052	1	CLNM	MOUSE	Q80tv1	mus musculu	797	7	3.2	1521	2	Q4RK84	TECTNG	Q4rk84	tetradodon n	
725	7	3.2	1074	2	Q82491	ARATH	Q82491	arabidopsis	798	7	3.2	1521	2	Q4RK84	TECTNG	Q4rk84	tetradodon n	
726	7	3.2	1079	2	Q5RQ44	BRARE	Q5rq44	brachydantio	799	7	3.2	1539	2	Q7R2Y4	GIALA	Q7r2y4	glardia lam	
727	7	3.2	1089	2	Q75B21	ASHGO	Q75b21	ashbya gos	800	7	3.2	1552	2	Q7R0S6	GIALA	Q7r0s6	glardia lam	
728	7	3.2	1091	2	Q8BDR7	STRB6	Q8bdr7	streplococc	801	7	3.2	1575	2	Q519G4	ENTHI	Q519g4	entamoeba h	
729	7	3.2	1091	2	Q970Q0	STRPN	Q97q0	streplococc	802	7	3.2	1603	2	Q54R77	DICDI	Q54r77	dictyosteli	
730	7	3.2	1096	2	Q4SP07	TECTNG	Q4sp07	tetradodon n	803	7	3.2	1617	2	Q527G3	MAGCR	Q527g3	magnaporthe	
731	7	3.2	1099	2	Q86ZJ5	PODAN	Q86zj5	podospora a	804	7	3.2	1620	2	Q5H962	HUMAN	Q5h962	homo sapien	
732	7	3.2	1100	2	Q9NV82	HUMAN	Q9nv82	homo sapien	805	7	3.2	1672	2	Q9Y1T1	TOXGO	Q9y1t1	toxoplasma	
733	7	3.2	1106	1	ITAT	RAT	Q63J58	rattus norv	806	7	3.2	1690	2	Q870V1	NEUCR	Q870v1	neurospora	
734	7	3.2	1119	2	Q54TT8	DICDI	Q54tt8	dictyosteli	807	7	3.2	1771	2	Q5DPT4	MOUSE	Q5dpt4	mus musculu	
735	7	3.2	1135	2	Q5H2X9	RAT	Q5h2x9	rattus norv	808	7	3.2	1796	2	Q4SLJ7	TECTNG	Q4slj7	tetradodon n	
736	7	3.2	1138	2	Q4SKZ1	TECTNG	Q4skz1	tetradodon n	809	7	3.2	1830	2	Q4SLJ7	TECTNG	Q4slj7	tetradodon n	
737	7	3.2	1146	2	Q8CH18	MOUSE	Q8ch18	mus musculu	810	7	3.2	1898	1	TRAY	HUMAN	TRAY	homo sapien	
738	7	3.2	1146	2	Q4RYK6	TECTNG	Q4ryk6	tetradodon n	811	7	3.2	1902	2	Q925Q1	MOUSE	Q925q1	mus musculu	
739	7	3.2	1150	2	Q6X935	HUMAN	Q6x935	homo sapien	812	7	3.2	1943	2	Q640Q1	MOUSE	Q640q1	mus musculu	
740	7	3.2	1150	2	Q8IX12	HUMAN	Q8ix12	homo sapien	813	7	3.2	1970	2	Q5VUI3	HUMAN	Q5vui3	homo sapien	
741	7	3.2	1150	2	Q5VUP6	HUMAN	Q5vup6	homo sapien	814	7	3.2	2047	2	Q601N7	MYCHY	Q601n7	mycoplasma	
742	7	3.2	1154	2	Q55C65	DICDI	Q55c65	dictyosteli	815	7	3.2	2075	2	Q4REJ8	TECTNG	Q4rej8	tetradodon n	
743	7	3.2	1157	2	Q64IG3	XENILA	Q64ig3	xenopus lae	816	7	3.2	2158	1	BAT2	MOUSE	BAT2	mus musculu	
744	7	3.2	1166	2	Q4IO90	GIBZE	Q4ig90	gibberella	817	7	3.2	2161	1	AR1A	HUMAN	AR1A	homo sapien	
745	7	3.2	1166	2	Q66219	PLAF7	Q66219	plasmodium	818	7	3.2	2285	1	OSU248	XENILA	OSu248	xenopus lae	
746	7	3.2	1178	2	Q6AHQ1	CABRL	Q6ahq1	caenorhabd1	819	7	3.2	2428	2	Q80ZV8	MOUSE	Q80zv8	mus musculu	
747	7	3.2	1179	1	ITAT	MOUSE	Q61J38	mus musculu	820	7	3.2	2429	2	Q80ZV8	MOUSE	Q80zv8	mus musculu	
748	7	3.2	1187	2	Q8BWG4	MOUSE	Q8bwg4	m mus muscu	821	7	3.2	2441	1	CBP	MOUSE	CBP	mus musculu	
749	7	3.2	1192	2	Q7KS05	DROME	Q7ks05	drosophila	822	7	3.2	2442	1	CBP	MOUSE	CBP	mus musculu	
750	7	3.2	1193	2	Q8IMU8	DROME	Q8imu8	drosophila	823	7	3.2	2442	1	Q6UH9	RAT	Q6uh9	homo sapien	
751	7	3.2	1193	2	Q8KJ29	BRILLO	Q8kj29	rhizobium 1	824	7	3.2	2472	2	Q4LEJ8	HUMAN	Q4lej8	homo sapien	
752	7	3.2	1207	2	Q4P3H6	USTMA	Q4p3h6	ustilago ma	825	7	3.2	2472	2	Q4S8B2	TECTNG	Q4s8b2	tetradodon n	
753	7	3.2	1208	2	Q96T49	HUMAN	Q96t49	homo sapien	826	7	3.2	2635	2	Q7WRU0	9NOST	Q7wru0	anabaena cl	
754	7	3.2	1216	2	Q482D6	TECTNG	Q482d6	tetradodon n	827	7	3.2	2635	2	Q7WRU0	9NOST	Q7wru0	anabaena cl	
755	7	3.2	1219	2	Q523G6	MAGCR	Q523g6	magnaporthe	828	7	3.2	2696	2	Q60WB1	CABER	Q60wb1	caenorhabd1	
756	7	3.2	1224	2	Q5BKU5	HUMAN	Q5bku5	homo sapien	829	7	3.2	2826	2	Q7S935	NEUCR	Q7s935	neurospora	
757	7	3.2	1227	2	Q96JW4	HUMAN	Q96jw4	homo sapien	830	7	3.2	2962	2	Q93326	CABEL	Q93326	caenorhabd1	
758	7	3.2	1239	2	Q5U2J6	XENILA	Q5u2j6	xenopus lae	831	7	3.2	3407	2	Q5H924	HUMAN	Q5h924	homo sapien	
759	7	3.2	1251	2	Q627P2	CAEBR	Q627p2	caenorhabd1	832	7	3.2	3586	2	Q7OKJ6	BACAM	Q7okj6	bacillus am	
760	7	3.2	1253	2	OSTEM5	HUMAN	OSTEM5	homo sapien	833	7	3.2	3593	2	Q4PEL1	USTMA	Q4pel1	ustilago ma	
761	7	3.2	1253	2	Q6B334	BRARE	Q6b334	brachydantio	834	7	3.2	3908	2	Q9BK91	STRPU	Q9bk91	strongyloce	

835	7	3.2	4037	2	Q4WPX3_ASEFU	Q4WPX3 aspergillus	908	6	2.7	66	2	Q6R5D6_MOUSE	Q6R5D6 mus musculus
836	7	3.2	4374	1	HUWE1_HUMAN	Q74627 homo sapien	909	6	2.7	67	1	SLYX_RHIL0	Q96W1 rhizobium 1
837	7	3.2	4374	2	Q4G222_HUMAN	Q4G222 homo sapien	910	6	2.7	67	2	Q97X56_SUTSO	Q97X56 sulfolobus
838	7	3.2	4374	2	Q4G221_MOUSE	Q4G221 mus musculu	911	6	2.7	67	2	Q7S1J2_NEUCR	Q7S1J2 neurospora
839	7	3.2	4377	1	HUWE1_MOUSE	Q71YH8 mus musculu	912	6	2.7	67	2	Q6C3M6_YARLI	Q6C3M6 yarrowia 1i
840	7	3.2	4378	2	Q4UG03_MOUSE	Q419G3 mus musculu	913	6	2.7	67	2	Q9VCP3_DROME	Q9VCP3 drosophila
841	7	3.2	4473	1	PLEC1_CRIGR	Q91I55 cricetulus	914	6	2.7	67	2	Q8GVJ8_9POAL	Q8GVJ8 agrostis ac
842	7	3.2	4687	1	PLEC1_HUMAN	Q15149 homo sapien	915	6	2.7	67	2	Q81X90_BACAN	Q81X90 bacillus an
843	7	3.2	4796	2	Q4Q363_LEIMA	P30427 rattus norv	916	6	2.7	67	2	Q6MBR3_PARUV	Q6MBR3 paracauland
844	7	3.2	6885	1	SYNE2_HUMAN	Q4Q363 leishmania	917	6	2.7	67	2	Q9V1Q7_SHIVI	Q9V1Q7 human immun
845	7	3.2	8348	2	Q4S6Y5_TETNG	Q4S6Y5 tetraodon n	918	6	2.7	68	2	Q5V4F7_HALVA	Q5V4F7 halocaula
846	7	3.2	8407	2	Q7RTM4_HUMAN	Q7RTM4 homo sapien	919	6	2.7	68	2	Q7UD59_SHIFL	Q7UD59 shigella fl
848	7	3.2	8654	2	Q5TYO5_BRARE	Q5TYO5 brachydactylo	920	6	2.7	69	2	Q512P0_CONLE	Q512P0 conus leopa
849	7	3.2	8797	1	SYNE1_HUMAN	Q81E91 homo sapien	921	6	2.7	69	2	Q6EP69_ORYSA	Q6EP69 oryza sativ
850	6	2.7	28	2	Q7RF66_PLAYO	Q7RF66 plasmodium	922	6	2.7	69	2	Q8BPM2_CORER	Q8BPM2 cornebacte
851	6	2.7	30	2	Q7RF64_PLAYO	Q7RF64 plasmodium	923	6	2.7	69	2	Q8QNG9_SPHYC	Q8QNG9 eotocarpus
852	6	2.7	38	2	Q16493_HUMAN	Q16493 homo sapien	924	6	2.7	70	2	Q84CV8_SBACT	Q84CV8 uncultured
853	6	2.7	30	2	Q4RAC9_TETNG	Q4RAC9 tetraodon n	925	6	2.7	70	2	Q6NHG3_CORDI	Q6NHG3 cytochrome
854	6	2.7	34	2	Q6B113_YEAST	Q6B113 saccharomyc	926	6	2.7	70	2	Q6UG85_YVIRU	Q6UG85 sulfolobus
855	6	2.7	34	2	Q7R125_PLAYO	Q7R125 plasmodium	927	6	2.7	70	2	Q8BC18_NPVEM	Q8BC18 bombix mori
856	6	2.7	36	2	Q5SJU3_THERT8	Q5SJU3 thermus the	928	6	2.7	71	2	Q8UP56_AGRTS	Q8UP56 agrobacteri
857	6	2.7	37	1	Q6D28_LUPAN	P09930 lupinus ang	929	6	2.7	71	2	Q7VB82_PROMM	Q7VB82 prochloroco
858	6	2.7	37	2	Q41794_SHIVI	Q41794 human immun	930	6	2.7	72	2	Q8LCW7_ARATH	Q8LCW7 arabidopsis
859	6	2.7	37	2	Q89598_SHIVI	Q89598 human immun	931	6	2.7	72	2	Q94A69_ARATH	Q94A69 arabidopsis
860	6	2.7	37	2	Q8UTU3_SHIVI	Q8UTU3 human immun	932	6	2.7	72	2	Q6HR26_BACAN	Q6HR26 bacillus an
861	6	2.7	37	2	Q89489_SHIVI	Q89489 human immun	933	6	2.7	72	2	Q4SUW2_TETNG	Q4SUW2 tetraodon n
862	6	2.7	37	2	Q8PXM6_SHIVI	Q8PXM6 human immun	934	6	2.7	72	2	Q8DUJ2_SHIVI	Q8DUJ2 human immun
863	6	2.7	37	2	Q8PXM7_SHIVI	Q8PXM7 human immun	935	6	2.7	73	2	Q8TLZ6_METAC	Q8TLZ6 mechanosarc
864	6	2.7	39	2	Q9GCF1_9GAMA	Q9GCF1 human herpe	936	6	2.7	73	2	Q8NEB9_HUMAN	Q8NEB9 homo sapien
865	6	2.7	40	2	Q6K180_MYCMO	Q6K180 mycoplasma	937	6	2.7	73	2	Q6LCK2_MOUSE	Q6LCK2 mus musculu
866	6	2.7	41	2	Q51371_SHIVI	Q51371 human immun	938	6	2.7	73	2	Q8AYX6_9GAMA	Q8AYX6 porcine lym
867	6	2.7	42	1	BD13_BOVIN	P46171 bos taurus	939	6	2.7	74	2	Q6B8C2_9ACAR	Q6B8C2 iordex paci
868	6	2.7	44	2	Q73KJ9_TREDE	Q73KJ9 treponema d	940	6	2.7	74	2	Q4YR44_PLABE	Q4YR44 plasmodium
869	6	2.7	45	1	SEPU_BACSU	Q7WY58 bacillus su	941	6	2.7	74	2	Q70B17_HDV	Q70B17 hepatitis d
870	6	2.7	45	2	Q5C4D6_SCHJA	Q5C4D6 schistosoma	942	6	2.7	75	2	Q8U397_PYRFU	Q8U397 pyrococcus
871	6	2.7	45	2	Q7RGN2_PLAYO	Q7RGN2 plasmodium	943	6	2.7	75	2	Q6CB05_YARLI	Q6CB05 yarrowia 1i
872	6	2.7	48	2	Q9ZGZ0_YERPE	Q9ZGZ0 yersinia pe	944	6	2.7	76	2	Q7X1J7_ORYSA	Q7X1J7 oryza sativ
873	6	2.7	48	2	Q74Y68_YERPE	Q74Y68 yersinia pe	945	6	2.7	76	2	Q8L9X5_ARATH	Q8L9X5 arabidopsis
874	6	2.7	48	2	Q8B517_STRAS	Q8B517 streptococc	946	6	2.7	76	2	Q83CM2_COXBU	Q83CM2 coxiella bu
875	6	2.7	49	2	Q6C0K4_YARLI	Q6C0K4 yarrowia 1i	947	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
876	6	2.7	49	2	Q605P1_METCA	Q605P1 methylococc	948	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
877	6	2.7	49	2	Q8TAB0_HUMAN	Q8TAB0 homo sapien	949	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
878	6	2.7	51	2	Q5JRR7_HUMAN	Q5JRR7 homo sapien	950	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
879	6	2.7	51	2	Q4YMG0_PLABE	Q4YMG0 plasmodium	951	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
880	6	2.7	51	2	Q5MEO0_BACSK	Q5MEO0 bacillus cl	952	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
881	6	2.7	52	2	Q5MEO8_BACSK	Q5MEO8 bacillus cl	953	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
882	6	2.7	52	2	Q92CD5_LISIN	Q92CD5 listeria in	954	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
883	6	2.7	52	2	Q804A3_PSEAM	Q804A3 pseudopleur	955	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
884	6	2.7	53	1	BDCT_BOVIN	Q18815 bos taurus	956	6	2.7	78	1	Q83CM2_COXBU	Q83CM2 coxiella bu
885	6	2.7	53	2	Q8PF63_LEPIN	Q8PF63 leptospira	957	6	2.7	79	2	Q6L1Z3_DROME	Q6L1Z3 drosophila
886	6	2.7	53	2	Q8PBM7_ECOL6	Q8PBM7 escherichia	958	6	2.7	79	2	Q5OWV6_ENTHI	Q5OWV6 entamoeba h
887	6	2.7	54	2	Q16031_HUMAN	Q16031 homo sapien	959	6	2.7	79	2	Q9ACB0_BRUBA	Q9ACB0 bruceella h
888	6	2.7	54	2	Q6UG86_YVIRU	Q6UG86 sulfolobus	960	6	2.7	79	2	Q5GS73_MOLTR	Q5GS73 wolbachia s
889	6	2.7	56	2	Q90175_SHIVI	Q90175 human immun	961	6	2.7	79	2	Q4T045_TETNG	Q4T045 tetraodon n
890	6	2.7	57	2	Q4M8Z2_ASFPU	Q4M8Z2 aspergillus	962	6	2.7	80	2	Q656V6_ORYSA	Q656V6 oryza sativ
891	6	2.7	58	2	Q26585_METTH	Q26585 methanobact	963	6	2.7	80	2	Q8LQ75_ORYSA	Q8LQ75 oryza sativ
892	6	2.7	58	2	Q4UVI0_CORUK	Q4UVI0 corynebacte	964	6	2.7	80	2	Q9KMW5_XANOR	Q9KMW5 xanthomonas
893	6	2.7	59	2	Q691T7_ORYSA	Q691T7 oryza sativ	965	6	2.7	80	2	Q62UJ4_BACLD	Q62UJ4 bacillus l
894	6	2.7	59	2	Q6TRU3_YVIRU	Q6TRU3 sulfolobus	966	6	2.7	80	2	Q4US45_XANCP	Q4US45 xanthomonas
895	6	2.7	60	2	Q71UAS_BOVIN	Q71UAS bos taurus	967	6	2.7	81	2	Q8PBA1_XANCP	Q8PBA1 xanthomonas
896	6	2.7	60	2	Q5M5G7_BOVIN	Q5M5G7 bos taurus	968	6	2.7	81	2	Q9YER1_AERPE	Q9YER1 aeropyrum p
897	6	2.7	63	2	Q68HX2_XANOR	Q68HX2 xanthomonas	969	6	2.7	81	2	Q61HT2_DROME	Q61HT2 drosophila
898	6	2.7	63	2	Q63NT8_BURPS	Q63NT8 burkholderi	970	6	2.7	82	2	Q93KQ2_TEREN	Q93KQ2 teres
899	6	2.7	65	2	Q6G9P1_STAAS	Q6G9P1 stephilococ	971	6	2.7	82	2	Q6EPV5_ORYSA	Q6EPV5 oryza sativ
900	6	2.7	65	2	Q6G889_STAAS	Q6G889 stephilococ	972	6	2.7	82	2	Q6GVDE_FFRAN	Q6GVDE fragaria an
901	6	2.7	65	2	Q7VA99_PROMA	Q7VA99 prochloroco	973	6	2.7	82	2	Q8VH78_MUSSA	Q8VH78 mus saxicol
902	6	2.7	65	2	Q5HG44_STAAC	Q5HG44 stephilococ	974	6	2.7	83	2	Q8VH78_MUSSA	Q8VH78 mus saxicol
903	6	2.7	65	2	Q7A100_STAAN	Q7A100 stephilococ	975	6	2.7	83	2	Q702Y6_MUSPA	Q702Y6 anopheles g
904	6	2.7	65	2	Q7ASUD_STAAN	Q7ASUD stephilococ	976	6	2.7	83	2	Q6K4B4_ORYSA	Q6K4B4 oryza sativ
905	6	2.7	65	2	Q99U99_STAAM	Q99U99 stephilococ	977	6	2.7	84	2	Q5ECA3_SHIVI	Q5ECA3 human immun
906	6	2.7	66	2	Q6CH60_YARLI	Q6CH60 yarrowia 1i	978	6	2.7	85	2	Q5VP42_ORYSA	Q5VP42 oryza sativ
907	6	2.7	66	2	Q5CKL9_CRYHO	Q5CKL9 cryptospori	979	6	2.7	85	2	Q5J7J4_ORYSA	Q5J7J4 oryza sativ
							980	6	2.7	85	2	Q9WMG1_XANCV	Q9WMG1 xanthomonas

981 6 2.7 86 1 Y1279_IACAC 05f15 lactobacill
982 6 2.7 86 2 Q4Y7K7_PLACH 04y7k7 plasmodium
983 6 2.7 86 2 Q48Y8_BACME 08y8y8 bacillus me
984 6 2.7 86 2 Q6MAH2_PAKOW 06mah2 paracitand
985 6 2.7 87 2 Q4J1M0_AZCVI 04j1m0 acotobacter
986 6 2.7 88 2 Q9T0Z7_9CAUD 09t0z7 bacterioph
987 6 2.7 88 2 Q6Q0Z8_HDV 06q0z8 hepatitis d
988 6 2.7 88 2 Q6Q0Z9_HDV 06q0z9 hepatitis d
989 6 2.7 88 2 Q6Q0R0_HDV 06q0r0 hepatitis d
990 6 2.7 88 2 Q74774_9H1V1 074774 human immun
991 6 2.7 89 2 Q6LY84_METMP 06ly84 methanococ
992 6 2.7 89 2 Q7V5S9_PROMM 07v5s9 prochloroc
993 6 2.7 89 2 Q35549_MUSSP 035549 mus sprecus
994 6 2.7 90 2 Q7VUC9_BORPE 07vuc9 bordelella
995 6 2.7 90 2 Q7W415_BORPA 07w415 bordelella
996 6 2.7 90 2 Q6PDY8_MOUSE 06pdy8 mus musculu
997 6 2.7 91 1 IIG1_CAEBL 01g060 caenorhadit
998 6 2.7 91 2 Q687Y5_9H1V1 0687y5 human immun
999 6 2.7 91 2 Q8US8_9H1V1 08us8 human immun
1000 6 2.7 92 2 Q5JW64_HUMAN 05jw64 homo sapien

ALIGNMENTS

RESULT 1
Q922V0_MOUSE PRELIMINARY; PRT; 220 AA.

AC Q922V0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Beta spectrin homolog.
GN Name=Spnb2; Synonym=SLF1;
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57 Black/6;
RA Cai T., Yu P., Mishra B., Mishra L.;

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
EMBL: AF016040; AAD01566.1; -; mRNA.
DR HSSP; Q15149; IMB8.

DR MGI; MGI:98388; Spnb2.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.

DR GO; GO:000515; F:protein binding; IPT.
DR GO; GO:0007182; P:common-partner SMAD protein phosphorylation; IDA.

DR GO; GO:0007184; P:SMAD protein nuclear translocation; IDA.
DR InterPro; IPR001589; Actbind_actin.

DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.

DR SMART; SM00033; CH; 1.

DR PROSITE; PS00019; ACTININ_1; 1.

DR PROSITE; PS50021; CH; 1.

DR SEQUENCE 220 AA; 25529 MW; F68CAB6A1E1F4253 CRC64;

Query Match 100.0%; Score 220; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No.2.5e-218;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEIORTSSISGIPSPAYTGQVYNYNQLDEGRFQLODEREAVQKPTTKVNSHLARVSC 60
DB 1 MEIORTSSISGIPSPAYTGQVYNYNQLDEGRFQLODEREAVQKPTTKVNSHLARVSC 60
QY 61 RITDLYLDADGKMLITLVLSEGERLPKPTKGMRHCHLENDKALQPKEDRVHLENN 120
DB 61 RITDLYLDADGKMLITLVLSEGERLPKPTKGMRHCHLENDKALQPKEDRVHLENN 120
QY 121 GSHDIYVGNHRLITLLELVRRQOEERERKRPPSPDPTKVSSEASQOWDTSKQDVS 180

DB 121 GSHDIYVGNHRLITLLELVRRQOEERERKRPPSPDPTKVSSEASQOWDTSKQDVS 180
QY 181 QNGIPAEQSGPRVYSRQTYQNYKNFNSRRTASHSNSGM 220
DB 181 QNGIPAEQSGPRVYSRQTYQNYKNFNSRRTASHSNSGM 220

RESULT 2
Q8C509_MOUSE PRELIMINARY; PRT; 155 AA.

AC Q8C509;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430088M03 product:beta-spectrin 2, non-erythrocytic,
full insert sequence. (Fragment).

DE full insert sequence. (Fragment).
GN Name=Spnb2;
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y., High-efficiency full-length cDNA cloning.,"
Meth. Enzymol. 303:19-44(1999).

RL Meth. Enzymol. 303:19-44(1999).

RN [2]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aikawa T., Hara A., Fukunishi Y., Kono H., Aachi U., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gasteierland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaez P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschütter S.,
Hayashizaki Y., Functional annotation of a full-length mouse cDNA collection.,"
Nature 409:685-690(2001).

RL Nature 409:685-690(2001).

RN [3]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.,"
Nature 420:563-573(2002).

RL Nature 420:563-573(2002).

RN [4]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.,"
Genome Res. 10:1617-1630(2000).

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus; DOI=10.1101/gr.152600;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shihata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachiiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichipillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaikawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK079842; BAC37762.1; -; mRNA.
 DR HSSP; Q15149; IMB8.
 DR MGI; MGI:98388; Spn2.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0005513; F:protein binding; IPI.
 DR GO; GO:0007182; P:common-partner SMAD protein phosphorylation; IDA.
 DR GO; GO:0007184; P:SMAD protein nuclear translocation; IDA.
 DR InterPro; IPR001589; Actbind actin.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 DR SMART; SM00033; CH; 1.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 1.
 DR FT NON TER 155 155
 DR SQ SEQUENCE 155 AA; 18020 MW; E9F58F25CA6BDF8 CRC64;
 Query Match 60.5%; Score 133; DB 2; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELQRTSSISGPLSPAYTGVPPYNNQLEGRFKQLQDEREAVQKTFKWNSHLARVSC 60
 DB 1 MELQRTSSISGPLSPAYTGVPPYNNQLEGRFKQLQDEREAVQKTFKWNSHLARVSC 60
 QY 61 RITDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHCLENVKALQFLKEQVRHLENN 120
 DB 61 RITDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHCLENVKALQFLKEQVRHLENN 120
 QY 121 GSHDIVDGNHRLT 133
 DB 121 GSHDIVDGNHRLT 133
 RESULT 3
 ID Q5SOL9 MOUSE PRELIMINARY; PRT; 2154 AA.
 AC Q5SOL9;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Spectrin beta 2.
 GN Name=Spn2; ORFNames=RP23-189P1.1-002;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Phillimore B.;
 RL Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Tronians A.;
 RL Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL731792; CA124366.1; -; Genomic DNA.
 DR EMBL; AL672225; CA125429.1; -; Genomic DNA.
 DR EMBL; AL731792; CA125429.1; JOINED; Genomic DNA.
 DR Ensembl; ENSMUSG0000020315; Mus musculus.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR001589; Actin actin bd.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00435; Spectrin; 17.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00150; SPEC; 17.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.
 DR SQ SEQUENCE 2154 AA; 251156 MW; 5128A840C3FD28AC CRC64;
 Query Match 60.5%; Score 133; DB 2; Length 2154;
 Best Local Similarity 100.0%; Pred. No. 1.6e-127;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELQRTSSISGPLSPAYTGVPPYNNQLEGRFKQLQDEREAVQKTFKWNSHLARVSC 60
 DB 1 MELQRTSSISGPLSPAYTGVPPYNNQLEGRFKQLQDEREAVQKTFKWNSHLARVSC 60
 QY 61 RITDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHCLENVKALQFLKEQVRHLENN 120
 DB 61 RITDLYTDLRGRMLIKLEVLSEGRLPKPTKGRMRHCLENVKALQFLKEQVRHLENN 120
 QY 121 GSHDIVDGNHRLT 133
 DB 121 GSHDIVDGNHRLT 133
 RESULT 4
 ID O8IX99 HUMAN PRELIMINARY; PRT; 2155 AA.
 AC O8IX99;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Beta-spectrin 2 isoform 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21521960; PubMed=1165863; DOI=10.1385/JMN.17.1:59;
 RA Chen Y., Yu P., Lu D., Tagle D.A., Cai T.;
 RT "A novel isoform of beta-spectrin II localizes to cerebellar Purkinje-
 RT cell bodies and interacts with neurofibromatosis type 2 gene product
 RT schwannomn.";
 RL J. Mol. Neurosci. 17:59-70(2001).
 DR EMBL; AF377441; AA015362.1; -; mRNA.
 DR HSSP; Q01082; IBKR.
 DR Ensembl; ENSG00000115306; Homo sapiens.
 DR GO; GO:0005856; C:cytoskeleton; IEA.
 DR GO; GO:0003779; F:actin binding; IEA.

DR InterPro: IPR001589; Acbind actin.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR002017; Spectrin.
DR Pfam: PF00307; CH_2.
DR Pfam: PF00435; Spectrin; 17.
DR SMART: SM00033; CH_2.
DR SMART: SM00150; SPEC; 17.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PS00020; ACTININ_2; 1.
DR PROSITE: PS00021; CH_2.
SQ SEQUENCE 2155 AA; 251418 MW; 20A91A28EAC0FBED CRC64;

Query Match	60.5%	Score 133	DB 2	Length 2155
Best Local Similarity	100.0%	Pred. No. 1.6e-127		
Matches 133	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	1	MELOQTSSISGSPSAFYGOVPEYNTNOLGFRKQLODEEAAVOKFTFTCMVNSHLARVSC	60
Db	1	MELOQTSSISGSPSAFYGOVPEYNTNOLGFRKQLODEEAAVOKFTFTCMVNSHLARVSC	60
Oy	61	RITDLYTLRPOGRMILKLENTSGERLPPPTGWRIRHGLEVDKALQELKORVHLEMM	120
Db	61	RITDLYTLRPOGRMILKLENTSGERLPPPTGWRIRHGLEVDKALQELKORVHLEMM	120
Oy	121	GSMDIVDGNHRLT	133
Db	121	GSMDIVDGNHRLT	133

RESULT 5	09OMJ7 MOUSE	09OMJ7 MOUSE PRELIMINARY;	PRT; 2154 AA.
ID	09OMJ7		
AC	01-MAY-2000 (TREMBlrel. 13. Created)		
DT	01-MAY-2000 (TREMBlrel. 13. Last sequence update)		
DT	01-OCT-2003 (TREMBlrel. 25. Last annotation update)		
DE	Non-erythrocyte beta spectrin.		
GN	Name=Spm2;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57 Black/6;		
RA	Cal T., Yu P., Mishra B., Monga P.S.P., Mishra L.;		
RL	Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF017112; AAD01616.1; -; mRNA.		
DR	HSSP; Q01082; 1BRK.		
DR	MGI; MGI:98388; Spn2.		
DR	GO; GO:0005634; C:nucleus; IDA.		
DR	GO; GO:0005886; C:plasma membrane; IDA.		
DR	GO; GO:0005515; F:protein binding; IPT.		
DR	GO; GO:0007185; P:common-partner SMD protein phosphorylation; IDA.		
DR	GO; GO:0007184; P:SMD protein nuclear translocation; IDA.		
DR	InterPro; IPR001589; Actbind actin.		
DR	InterPro; IPR001715; Calponin-like.		
DR	InterPro; IPR002017; Spectrin.		
DR	PIfam; PF00307; CH; 2.		
DR	PIfam; PF00435; Spectrin; 17.		
DR	SMART; SMO0035; CH; 2.		
DR	SMART; SMO0150; SPEC; 17.		
DR	PROSITE; PS00019; ACTININ_1; 1.		
DR	PROSITE; PS00020; ACTININ_2; 1.		
DR	PROSITE; PS50021; CH; 2.		
SEQ	SEQUENCE 2154 AA; 250928 MW; 872CFEC9C332152C CRC64;		

Query Match	56.4%	Score 124	DB 2	Length 2154
Best Local Similarity	100.0%	Pred. No. 3.2e+18		
Matches 124	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	10	SGPLSPATYGYPPYNTNQLGGRFKQLQDEREAVQKTKFTKWNSHARVSCRITDLYDL	69	

D _b	10	SGPLSPATGYQVPYNNOLGFRKQLOADERAVQPKPTFKVNSHLRVSCRITDLYTDL	69
Q _y	70	RDRMLIKLLEVLSEGRLLPKPTKGMRLTHCLLENVDKALQFLKEORVHLENMGSHDIVDGN	129
D _b	70	RDRMLIKLLEVLSEGRLLPKPTKGMRLTHCLLENVDKALQFLKEORVHLENMGSHDIVDGN	129
Q _y	130	HRLLT	133
D _b	130	HRLLT	133

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RESULT 6
06V0G7 CANFA
ID 06V0G7_CANFA PRELIMINARY; PRT; 149 AA.
AC 06V0G7;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, last annotation update)
DE Beta-spectrin (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mishra S., Sabbah H.N., Undrovinas A.I.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDDB databases.
DR EMBL; AY356552; AA063500.1; -; mRNA.
DR Ensembl; ENSGACFG00000002744; Canis familiaris.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind actinin.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR SMART; SM00033; CH; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PSS0021; CH; 1.
FT NON TER 149 149
SQ SEQUENCE 149 AA; 17412 MW; 2281545132D85CC CRC64;

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[illegible]

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RESULT 7
OSDTR4 MOUSE
ID OSDTR4_1
AC OSDTR4_1
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE MKIAA049 protein (Fragment).
GN Name=Spn2; Synonyms=MKIAA049;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI TaxID=10090;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain:
RC Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
RA Koga H.;

```


RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
 RT The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
 RT Identified by Screening of Terminal sequences of cDNA Clones Randomly
 RT Sampled from Size-Fractionated Libraries.";
 RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AK220456; BAD90485.1; -; mRNA.
 DR MGI; MGI:98388; Snpb2.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007184; P:common-partner SMAD protein phosphorylation; IDA.
 DR GO; GO:0007184; P:SMAD protein nuclear translocation; IDA.
 DR InterPro; IPR001589; Acbind actin.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00435; Spectrin; 9.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00150; SPEC; 9.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 1290 AA; 150490 MW; D9E1CD33E6AB299B CRC64;
 Query Match 44.1%; Score 97; DB 2; Length 1290;
 Best Local Similarity 100.0%; Pred. No. 1.5e-90;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 DEREAQKKTFTKWNVSHLAVSCLTDLTYDLRDGRMLIKLEVLGSGRLPKPTKGMNR 96
 DB 59 DEREAQKKTFTKWNVSHLAVSCLTDLTYDLRDGRMLIKLEVLGSGRLPKPTKGMNR 118
 QY 97 IHCLENVDKALQFLKEQVHLENMGSHDIVDGNHRLT 133
 DB 119 IHCLENVDKALQFLKEQVHLENMGSHDIVDGNHRLT 155
 RESULT 8
 Q6XD99_RAT PRELIMINARY; PRT; 2358 AA.
 ID Q6XD99; RAT
 AC Q6XD99;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Non-erythroid spectrin beta.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus;
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Chen Y., Huang C.-H.;
 RL Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AY238344; AA002380.1; -; mRNA.
 DR HSSP; Q01082; 1A2.
 DR SMR; Q6XD99; 2194-2299.
 DR Ensembl; ENSRNOG000005434; Rattus norvegicus.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR001589; Actinin actin bd.
 DR InterPro; IPR001715; Calponin act_Dd.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR002017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00435; Spectrin; 9.
 DR Pfam; PF00633; CH; 2.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00150; SPEC; 17.

DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 KW Actin capring; Actin-binding; Cytoskeleton.
 SQ SEQUENCE 2358 AA; 273586 MW; 625285A560453CC8 CRC64;
 Query Match 44.1%; Score 97; DB 2; Length 2358;
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 DEREAQKKTFTKWNVSHLAVSCLTDLTYDLRDGRMLIKLEVLGSGRLPKPTKGMNR 96
 DB 50 DEREAQKKTFTKWNVSHLAVSCLTDLTYDLRDGRMLIKLEVLGSGRLPKPTKGMNR 109
 QY 97 IHCLENVDKALQFLKEQVHLENMGSHDIVDGNHRLT 133
 DB 110 IHCLENVDKALQFLKEQVHLENMGSHDIVDGNHRLT 146
 RESULT 9
 SPTB2_MOUSE STANDARD; PRT; 2363 AA.
 ID SPTB2_MOUSE
 AC Q62261;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Spectrin beta chain, brain I (Spectrin, non-erythroid beta chain I)
 DE (Beta-II spectrin) (Fodrin beta chain)
 GN Name=Sptb1; Synonyms=Snb-2, Snpb2, Sptb2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA MEDLINE=93240985; PubMed=8479293; DOI=10.1016/0166-328X(93)90176-P;
 RA Ma Y., Zimmer W.B., Riederer B.M., Goodman S.R.;
 RT "The complete amino acid sequence for brain beta spectrin (beta fodrin): relationship to globin sequences.";
 RL Brain Res. Mol. Brain Res. 18:87-89(1993).
 RN [2]
 RP PHOSPHORYLATION SITES SER-1918, SER-2115, SER-2137 AND SER-2168.
 RA PubMed=15572359; DOI=10.1074/jbc.M411220200;
 RA Collins M.O., Yu L., Caba M.P., Husi H., Campuzano I.;
 RA Blackstock W.P., Choudhary J.S., Grant S.G.;
 RT "Proteomic analysis of in vivo phosphorylated synaptic proteins.";
 RL J. Biol. Chem. 280:5972-5982(2005).
 RN [3]
 RP STRUCTURE BY NMR OF 2199-2304.
 RA MEDLINE=94268558; PubMed=8208297; DOI=10.1038/36967580;
 RA Macias M.J., Musacchio A., Ponsingl H., Nilges M., Saraste M.,
 RA Osochkinat H.;
 RT "Structure of the pleckstrin homology domain from beta-spectrin.";
 RL Nature 369:675-677(1994).
 RN [4]
 RP STRUCTURE BY NMR OF 2199-2304.
 RA MEDLINE=97342712; PubMed=9199409; DOI=10.1006/jmbi.1997.1044;
 RA Nilges M., Macias M.J., O'Donoghue S.I., Osochkinat H.;
 RT "Automated NOESY interpretation with ambiguous distance restraints:
 the refined NMR solution structure of the pleckstrin homology domain
 from beta-spectrin.";
 RL J. Mol. Biol. 269:408-422(1997).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2199-2304.
 RA MEDLINE=96030773; PubMed=7589597;
 RA Hyvoenen M., Macias M.J., Nilges M., Osochkinat H., Saraste M.,
 RA Wilmanns M.;
 RT "Structure of the binding site for inositol phosphates in a PH
 domain.";
 RL EMBO J. 14:4676-4681(1995).

CC -1- FUNCTION: Fodrin, which seems to be involved in secretion,
 CC interacts with calmodulin in a calcium-dependent manner and is
 CC thus candidate for the calcium-dependent movement of the
 CC cytoskeleton at the membrane.
 CC -1- SUBUNIT: Like erythrocyte spectrin, the spectrin-like proteins are
 CC capable to form dimers which can further associate to tetramers.
 CC -1- SIMILARITY: Belongs to the spectrin family.
 CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 17 spectrin repeats.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, M74773; AAC2040.1; -; mRNA.
 CC PDB, 1BTN; X-ray; @=2199-2304.
 CC DR Intact; Q62261; -;
 CC DR Ensembl; ENSMUSG0000020315; Mus musculus.
 CC MGI; MGI:98388; Spn2.
 CC DR GO; GO:0005634; C:nucleus; IDA.
 CC DR GO; GO:0005886; C:plasma membrane; IDA.
 CC DR GO; GO:0005515; F:protein binding; IPI.
 CC DR GO; GO:0007182; P:common-partner SMAD protein phosphorylation; IDA.
 CC DR GO; GO:0007184; P:SMAD protein nuclear translocation; IDA.
 CC DR InterPro; IPR001589; Actinin actin bd.
 CC DR InterPro; IPR001715; Calponin_act_bd.
 CC DR InterPro; IPR011849; PH.
 CC DR InterPro; IPR011993; PH type.
 CC DR InterPro; IPR02017; Spectrin.
 CC DR InterPro; IPR01605; Spectrin_PH.
 CC DR Pfam; PF00307; CH; 2.
 CC DR Pfam; PF00169; PH; 1.
 CC DR Pfam; PF00435; Spectrin; 16.
 CC DR PRINTS; PR00683; SPECTRINPH.
 CC DR PROSITE; PS00019; ACTININ_1; 1.
 CC DR PROSITE; PS00020; ACTININ_2; 1.
 CC DR PROSITE; PS50021; CH; 2.
 CC DR PROSITE; PS50003; PH_DOMAIN; 1.
 CC DR 3D-structure; Actin capping; Actin-binding; Calmodulin-binding;
 CC Cytoskeleton; Membrane; Phosphorylation; Repeat.
 CC KM CYTOSKELETON; Membrane; Phosphorylation; Repeat.
 CC FT DOMAIN 1 275 Actin-binding (By similarity).
 CC FT 54 158 CH 1.
 CC FT 173 275 CH 2.
 CC FT REPEAT 276 384 Spectrin 1.
 CC FT REPEAT 385 498 Spectrin 2.
 CC FT REPEAT 499 608 Spectrin 3.
 CC FT REPEAT 609 714 Spectrin 4.
 CC FT REPEAT 715 819 Spectrin 5.
 CC FT REPEAT 820 925 Spectrin 6.
 CC FT REPEAT 926 1032 Spectrin 7.
 CC FT REPEAT 1033 1145 Spectrin 8.
 CC FT REPEAT 1140 1245 Spectrin 9.
 CC FT REPEAT 1246 1350 Spectrin 10.
 CC FT REPEAT 1351 1462 Spectrin 11.
 CC FT REPEAT 1463 1562 Spectrin 12.
 CC FT REPEAT 1563 1668 Spectrin 13.
 CC FT REPEAT 1669 1775 Spectrin 14.
 CC FT REPEAT 1776 1881 Spectrin 15.
 CC FT REPEAT 1882 1987 Spectrin 16.
 CC FT REPEAT 1988 2132 Spectrin 17.
 CC FT DOMAIN 2136 2306 PH.
 CC FT MOD_RES 2196 2306 Phosphoserine.
 CC FT MOD_RES 2115 2115 Phosphoserine.
 CC FT MOD_RES 2127 2127 Phosphoserine (By similarity).
 CC FT MOD_RES 2137 2137 Phosphoserine.
 CC FT MOD_RES 2164 2164 Phosphoserine (By similarity).
 CC FT MOD_RES 2168 2168 Phosphoserine.
 CC STRAND 2200 2209
 CC TURN 2212 2213

FT STRAND 2215 2215
 FT STRAND 2222 2229
 FT TURN 2230 2231
 FT STRAND 2232 2236
 FT STRAND 2239 2244
 FT TURN 2245 2245
 FT STRAND 2254 2255
 FT TURN 2257 2258
 FT STRAND 2260 2263
 FT STRAND 2273 2277
 FT TURN 2279 2280
 FT STRAND 2283 2287
 FT HELIX 2291 2303
 SQ SEQUENCE 2363 AA; 274422 MW; 64C9EABD26B8C7B8 CRC64;
 Query Match 44.1%; Score 97; DB 1; Length 2363;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-90;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 DERAAVQKKTFTKWNHSHARVSCRTDLYTDLRDGRMLIKLLEVLGGERLPKPTKGRMR 96
 DB 50 DERAAVQKKTFTKWNHSHARVSCRTDLYTDLRDGRMLIKLLEVLGGERLPKPTKGRMR 109
 QY 97 IHCLENVDKALQFLKEQVRHLENNGSHDIYDGNRLT 133
 DB 110 IHCLENVDKALQFLKEQVRHLENNGSHDIYDGNRLT 146
 RESULT 10
 Q55QJ8_MOUSE Q55QJ8_MOUSE PRELIMINARY; PRT; 2363 AA.
 AC Q55QJ8;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Spectrin beta 2.
 GN Name=Spn2; ORFNames=RP23-189P1.1-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Philimore B.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Trotman A.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC EMBL; AL731792; CA124367.1; -; Genomic DNA.
 CC EMBL; AL672225; CA125430.1; -; Genomic DNA.
 CC EMBL; AL672225; CA124367.1; JOINED; Genomic DNA.
 CC EMBL; AL731792; CA125430.1; JOINED; Genomic DNA.
 CC SMR; Q55QJ8; 2199-2304.
 CC DR Ensembl; ENSMUSG0000020315; Mus musculus.
 CC DR GO; GO:0003779; F:actin binding; IEA.
 CC DR InterPro; IPR001589; Actinin actin bd.
 CC DR InterPro; IPR001715; Calponin_act_bd.
 CC DR InterPro; IPR001849; PH.
 CC DR InterPro; IPR011993; PH type.
 CC DR InterPro; IPR02017; Spectrin.
 CC DR InterPro; IPR01605; Spectrin_PH.
 CC DR Pfam; PF00307; CH; 2.
 CC DR Pfam; PF00169; PH; 1.
 CC DR Pfam; PF00435; Spectrin; 17.
 CC DR PRINTS; PR00683; SPECTRINPH.
 CC DR SMART; SM00033; CH; 2.
 CC DR SMART; SM00233; PH; 1.
 CC DR SMART; SM00150; SPEC; 17.
 CC DR PROSITE; PS00019; ACTININ_1; 1.
 CC DR PROSITE; PS00020; ACTININ_2; 1.

DR PROSITE; PS50021; CH; 2.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 KW Actin capping; Actin-binding; Cytoskeleton.
 SO SEQUENCE 2363 AA; 274223 MW; 2213620545E4B8C CRC64;

Query Match: 44.1%; Score 97; DB 2; Length 2363;
 Best Local Similarity 100.0%; Pred. No. 2,7e-90;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 DERAVQKRTTKWNSHARVSCRTITLTYDLRGRMLIKLEVLSEERLPKPKGMR 96
 DB 50 DERAVQKRTTKWNSHARVSCRTITLTYDLRGRMLIKLEVLSEERLPKPKGMR 109
 QY 97 IHCLENVDKALQFLKEGRVHLENMGSHDIVDGNHRLT 133
 DB 110 IHCLENVDKALQFLKEGRVHLENMGSHDIVDGNHRLT 146

RESULT 11
 SPTB2 HUMAN STANDARD; PRT; 2364 AA.
 AC Q01082; O60837; Q16057;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1)
 DE (Beta-II spectrin) (Fodrin beta chain)
 GN Name=SPTB1; Synonyms=SPTB2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE (ISOFORM LONG).
 RX TISSUE=Brain;
 RX MEDLINE=92406787; PubMed=1527002;
 RA Hu R.J., Watanabe M., Bennett V.;
 RT "Characterization of human brain cDNA encoding the general isoform of
 RT beta-spectrin.";
 RL J. Biol. Chem. 267:18715-18722(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 293-1544.
 RP MEDLINE=94010920; PubMed=8406479;
 RA Chang J.G., Scarpa A., Eddy R.L., Byers M.G., Harris A.S.,
 RA Morrow J.S., Watkins P., Shows T.B., Forget B.G.;
 RT "Cloning of a portion of the chromosomal gene and cDNA for human beta-
 RT fodrin, the nonerythroid form of beta-spectrin.";
 RL Genomics 17:287-293(1993).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 2087-2168 (ISOFORM SHORT).
 RP TISSUE=Skeletal muscle;
 RX MEDLINE=20267884; PubMed=10806113;
 RA Hayes N.V.L., Scott C., Heerkes E., Ochanian V., Magge A.M.,
 RA Pinder J.C., Kordeli E., Baines A.J.;
 RT "Identification of a novel C-terminal variant of beta1 spectrin: two
 RT isoforms of beta1 spectrin have distinct intracellular locations and
 RT activities.";
 RL J. Cell Sci. 113:2023-2034(2000).
 RN [4]
 RP PHOSPHORYLATION SITES SRR-2128; SRR-2138; SRR-2165 AND SRR-2169.
 RX PubMed15502935; DOI=10.1073/pnas.0404720101;
 RA Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
 RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
 RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 173-280.
 RX MEDLINE=97307247; PubMed=9164454;
 RA Carugo K.D., Bannetlo S., Saraste M.;
 RT "Crystal structure of a calponin homology domain.";
 RL Nat. Struct. Biol. 4:175-179(1997).
 RN [6]

RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 173-281.
 RX MEDLINE=99036861; PubMed=9817844; DOI=10.1016/S0969-2126(98)00141-5;
 RA Bannetlo S., Saraste M., Carugo K.D.;
 RT "Structural comparisons of calponin homology domains: implications for
 RT actin binding.";
 RL Structure 6:1419-1431(1998).
 CC -1 FUNCTION: Fodrin, which seems to be involved in secretion,
 CC interacts with calmodulin in a calcium-dependent manner and is
 CC thus candidate for the calcium-dependent movement of the
 CC cytoskeleton at the membrane.
 CC -1 SUBUNIT: Like erythrocyte spectrin, the spectrin-like proteins are
 CC capable to form dimers which can further associate to tetramers.
 CC The short form cannot bind to the axonal protein fodaxin.
 CC -1 ALTERNATIVE PRODUCTS:
 CC Name=Long;
 CC IsoId=Q01082-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=Q01082-2; Sequence=VSP_000720, VSP_000721;
 CC -1 SIMILARITY: Belongs to the spectrin family.
 CC -1 SIMILARITY: Contains 2 CH (calponin-homology) domains.
 CC -1 SIMILARITY: Contains 1 PH domain.
 CC -1 SIMILARITY: Contains 17 spectrin repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; M96803; AAA60580.1; -; mRNA.
 CC EMBL; S65762; AAB28324.1; -; mRNA.
 CC EMBL; AJ005634; CAA06678.1; -; mRNA.
 CC EMBL; AJ238723; CAB91088.1; -; Genomic_DNA.
 CC PIR; A44159; A44159.
 CC PIR; A47213; A47213.
 CC PDB; 1AA2; X-ray; @=173-280.
 CC PDB; 1BKR; X-ray; A=172-280.
 CC SRR; Q01082; 2200-2305.
 CC InAct; Q01082; -;
 CC Ensembl; ENSG00000115306; Homo sapiens.
 CC HGNC; HGNC:11275; SPTB1.
 CC MIM; 182790; -;
 CC GO; GO:0008091; C:spectrin; TAS.
 CC GO; GO:0003779; F:actin binding; TAS.
 CC GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
 CC InterPro; IPR001589; Actinin actin bd.
 CC InterPro; IPR001715; Calponin_act_bd.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR011993; PH_type.
 CC InterPro; IPR002017; Spectrin.
 CC InterPro; IPR001605; Spectrin_PH.
 CC Pfam; PF00307; CH; 2.
 CC Pfam; PF00169; PH; 1.
 CC Pfam; PF00435; Spectrin; 17.
 CC PRINTS; PR00683; SPECTRINPH.
 CC PROSITE; PS00019; ACTININ_1; 1.
 CC PROSITE; PS00020; ACTININ_2; 1.
 CC PROSITE; PS50021; CH; 2.
 CC PROSITE; PS50003; PH DOMAIN; 1.
 CC 3D-structure; Actin capping; Actin-binding; Alternative splicing;
 CC Calmodulin-binding; Cytoskeleton; Membrane; Phosphorylation; Repeat.
 CC Calmodulin-binding; Cytoskeleton; Membrane; Phosphorylation; Repeat.
 CC Actin-binding (By similarity).
 FT DOMAIN 1 158
 FT DOMAIN 2 173
 FT DOMAIN 3 275
 FT DOMAIN 4 384
 FT DOMAIN 5 498
 FT DOMAIN 6 608
 FT DOMAIN 7 714
 FT DOMAIN 8 820
 FT DOMAIN 9 925
 FT DOMAIN 10 1032
 FT DOMAIN 11 1139

FT	REPEAT	1140	1245	Spectrin 9.
FT <td>REPEAT</td> <td>1246</td> <td>1350</td> <td>Spectrin 10.</td>	REPEAT	1246	1350	Spectrin 10.
FT <td>REPEAT</td> <td>1351</td> <td>1462</td> <td>Spectrin 11.</td>	REPEAT	1351	1462	Spectrin 11.
FT <td>REPEAT</td> <td>1463</td> <td>1562</td> <td>Spectrin 12.</td>	REPEAT	1463	1562	Spectrin 12.
FT <td>REPEAT</td> <td>1563</td> <td>1668</td> <td>Spectrin 13.</td>	REPEAT	1563	1668	Spectrin 13.
FT <td>REPEAT</td> <td>1669</td> <td>1775</td> <td>Spectrin 14.</td>	REPEAT	1669	1775	Spectrin 14.
FT <td>REPEAT</td> <td>1776</td> <td>1881</td> <td>Spectrin 15.</td>	REPEAT	1776	1881	Spectrin 15.
FT <td>REPEAT</td> <td>1882</td> <td>1987</td> <td>Spectrin 16.</td>	REPEAT	1882	1987	Spectrin 16.
FT <td>REPEAT</td> <td>1988</td> <td>2133</td> <td>Spectrin 17.</td>	REPEAT	1988	2133	Spectrin 17.
FT <td>DOMAIN</td> <td>2197</td> <td>2307</td> <td>PH.</td>	DOMAIN	2197	2307	PH.
FT <td>MOD_RES</td> <td>1918</td> <td>1918</td> <td>Phosphoserine (By similarity).</td>	MOD_RES	1918	1918	Phosphoserine (By similarity).
FT <td>MOD_RES</td> <td>2115</td> <td>2115</td> <td>Phosphoserine (By similarity).</td>	MOD_RES	2115	2115	Phosphoserine (By similarity).
FT <td>MOD_RES</td> <td>2128</td> <td>2128</td> <td>Phosphoserine.</td>	MOD_RES	2128	2128	Phosphoserine.
FT <td>MOD_RES</td> <td>2138</td> <td>2138</td> <td>Phosphoserine.</td>	MOD_RES	2138	2138	Phosphoserine.
FT <td>MOD_RES</td> <td>2165</td> <td>2165</td> <td>Phosphoserine.</td>	MOD_RES	2165	2165	Phosphoserine.
FT <td>MOD_RES</td> <td>2169</td> <td>2169</td> <td>Phosphoserine.</td>	MOD_RES	2169	2169	Phosphoserine.
FT <td>VARSPLIC</td> <td>2141</td> <td>2168</td> <td>MEATVDTISMVNGATEORTSKESPP -> VASRSQTQV NYNPNFSRRRTADQPMSCG (1n isoform Short). /Frid-VSP_000720. Missing (1n isoform Short). /Frid-VSP_000721. H -> D (1n Ref. 2).</td>	VARSPLIC	2141	2168	MEATVDTISMVNGATEORTSKESPP -> VASRSQTQV NYNPNFSRRRTADQPMSCG (1n isoform Short). /Frid-VSP_000720. Missing (1n isoform Short). /Frid-VSP_000721. H -> D (1n Ref. 2).
FT <td>VARSPLIC</td> <td>2169</td> <td>2364</td> <td></td>	VARSPLIC	2169	2364	
FT <td>CONFLICT</td> <td>1411</td> <td>1411</td> <td></td>	CONFLICT	1411	1411	
FT <td>HELIX</td> <td>174</td> <td>186</td> <td></td>	HELIX	174	186	
FT <td>TURN</td> <td>187</td> <td>189</td> <td></td>	TURN	187	189	
FT <td>TURN</td> <td>191</td> <td>192</td> <td></td>	TURN	191	192	
FT <td>HELIX</td> <td>200</td> <td>202</td> <td></td>	HELIX	200	202	
FT <td>TURN</td> <td>203</td> <td>204</td> <td></td>	TURN	203	204	
FT <td>HELIX</td> <td>206</td> <td>215</td> <td></td>	HELIX	206	215	
FT <td>HELIX</td> <td>217</td> <td>219</td> <td></td>	HELIX	217	219	
FT <td>HELIX</td> <td>222</td> <td>224</td> <td></td>	HELIX	222	224	
FT <td>TURN</td> <td>227</td> <td>228</td> <td></td>	TURN	227	228	
FT <td>HELIX</td> <td>230</td> <td>245</td> <td></td>	HELIX	230	245	
FT <td>HELIX</td> <td>253</td> <td>256</td> <td></td>	HELIX	253	256	
FT <td>HELIX</td> <td>263</td> <td>277</td> <td></td>	HELIX	263	277	
FT <td>TURN</td> <td>278</td> <td>278</td> <td></td>	TURN	278	278	
SO <td>SEQUENCE</td> <td>2364 AA; 274631 MW; 0122BD3DF25872CC CRC64;</td> <td></td> <td></td>	SEQUENCE	2364 AA; 274631 MW; 0122BD3DF25872CC CRC64;		

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Query Match          44.1%; Score 97; DB 1; Length 2364;
Best Local Similarity 100.0%; Pred.No. 2.7e-90;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 DEREAVQKTFPTKWNVNSHLARVSCSITLDYTLRDGRMIKLEVLSGERLKPPTKGMNR 96
      DERENQKTFPTKWNVNSHLARVSCSITLDYTLRDGRMIKLEVLSGERLKPPTKGMNR 109
Db 50 DEREAVQKTFPTKWNVNSHLARVSCSITLDYTLRDGRMIKLEVLSGERLKPPTKGMNR 109
      DERENQKTFPTKWNVNSHLARVSCSITLDYTLRDGRMIKLEVLSGERLKPPTKGMNR 133
Oy 97 IHCLENVDKALQFLKEQRYVHLENMGSHDIVDGNHRLT 133
      IHCLENVDKALQFLKEQRYVHLENMGSHDIVDGNHRLT 146
Db 110 IHCLENVDKALQFLKEQRYVHLENMGSHDIVDGNHRLT 146

RESULT 12
O59ER3_HUMAN
ID O59ER3_HUMAN PRELIMINARY; PRT; 2377 AA.
AC O59ER3;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, last annotation update)
DE Spectrin, beta, non-erythrocytic 1 isoform 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
CC 1. SIMILARITY: Contains 1 PH domain.
DR EMBL; AB209748; BAD92985.1; -; mRNA.
DR SMR; O59ER3; 2213-2318.

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DR	GO; GO:0003779; F-actin binding; IEA.
DR	InterPro; IPR001589; Actinin actin ID.
DR	InterPro; IPR001715; Calponin_act_bd.
DR	InterPro; IPR001449; PH.
DR	InterPro; IPR002017; Spectrin.
DR	InterPro; IPR001605; Spectrin_PH.
DR	Pfam; PF00307; CH; 2.
DR	Pfam; PF00169; PH; 1.
DR	Pfam; PF00435; Spectrin; 17.
DR	PRINTS; PR00683; SPECTRINPH.
DR	SMART; SM00033; CH; 2.
DR	SMART; SM00233; PH; 1.
DR	SMART; SM00150; SPEC; 17.
DR	PROSITE; PS00019; ACTININ_1; 1.
DR	PROSITE; PS00020; ACTININ_2; 1.
DR	PROSITE; PS50021; CH; 2.
DR	PROSITE; PS50003; PH_DOMAIN; 1.
KW	Actin capping; Actin-binding.
FT	NON_TER
SQ	SEQUENCE 2337 AA; 276170 MW; E4937200876298877 CRC64

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Query Match Similarity      44.1%; Score 97; DB 2; Length 2377;
Beet Local Similarity      100.0%; Pred. No. 2.8e-90;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Dd      63 DEREAVQKKTITKWNVNSHARVSCRTDLYTDLRDGRMLIKILEVLSGERLPKPTKGRMR 96
          97; Conservative 0; Mismatches 0; Indels 0; Gaps 0
          122 DEREAVQKKTITKWNVNSHARVSCRTDLYTDLRDGRMLIKILEVLSGERLPKPTKGRMR 122

Qy      97 IHCLENVDKALQFLKEQRVHLNNGSHDIVDGNHRLT 133
          123 IHCLENVDKALQFLKEQRVHLNNGSHDIVDGNHRLT 159

RESULT 13
O53R99 HUMAN
ID      O53R99 HUMAN PRELIMINARY; PRT; 2314 AA.
AC      O53R99
DT      13-SEP-2005 (TREMBLrel. 31, Created)
DT      13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE      Hypothetical protein SPTBN1 (Fragment).
GN      Name=SPTBN1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC      Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Kozlovicz A., Spalding L., Mulvaney E.;
RT      "The sequence of Homo sapiens BAC clone RP11-564H16."
RL      Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Waterston R.H.;
RT      Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RA      Waterston R.;
RT      Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RA      Wilson R.K.;
RT      Submitted (APR-2005) to the EMBL/GenBank/DBSJ databases.
CC      -1. SIMILARITY: Contains 1 PH domain.
DR      EMBL; AC093110; AY24229.1; -; Genomic_DNA.
DR      GO; GO:0003779; F:actin binding; IEA.
DR      InterPro; IPR001589; Actinin_actin_bd.
DR      InterPro; IPR001715; Calpoinn_act_bd.
DR      InterPro; IPR001849; PH.
DR      InterPro; IPR002017; Spectrin.

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DR Interpro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00435; Spectrin_17.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00150; SPEC; 17.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR Actin caping; Actin-binding; Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 2314 AA; 268716 MW; 9C49E79CFAD22081 CRC64;
 Query Match 43.6%; Score 96; DB 2; Length 2314;
 Best Local Similarity 100.0%; Pred. No. 2.9e-89;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 38 ERENQKTFKWNHSHARVSCRTDLYTDLRQGRMLIKLEVLSEGRLPKPTKGRRI 97
 Db 1 ERENQKTFKWNHSHARVSCRTDLYTDLRQGRMLIKLEVLSEGRLPKPTKGRRI 60
 Qy 98 HLENDVKALQFLKEQVHLENMGSHDIVDGNHRLT 133
 Db 61 HLENDVKALQFLKEQVHLENMGSHDIVDGNHRLT 96
 RESULT 14
 ID 0502M3 BRARE PRELIMINARY; PRT; 977 AA.
 AC 0502M3
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE LOC553451 protein (Fragment).
 GN Name=LOC553451;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shemen C.M., Schuler G.D.,
 RA Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantini P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumatre P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck R.A.,
 RA Villalón D.K., Muzny D.E., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Olfactory epithelium;
 RG NIH GSC Project;
 RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC095643; AA095643.1; -, mRNA.

FT NON TER 977 977
 SQ SEQUENCE 977 AA; 113881 MW; 5CC81C094A58BD01 CRC64;
 Query Match 30.0%; Score 66; DB 2; Length 977;
 Best Local Similarity 100.0%; Pred. No. 1.2e-58;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 68 DLRDGRMLIKLEVLSEGRLPKPTKGRMRHCLNVDKALQFLKEQVHLENMGSHDIVD 127
 Db 80 DLRDGRMLIKLEVLSEGRLPKPTKGRMRHCLNVDKALQFLKEQVHLENMGSHDIVD 139
 Qy 128 GNRHL 133
 Db 140 GNRHL 145
 RESULT 15
 ID 04REP5 TETNG PRELIMINARY; PRT; 2235 AA.
 AC 04REP5
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 10 SCAF15123, whole genome shotgun sequence.
 GN ORNames=STENG00035677001;
 OS Tetradodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodon.
 NC NCB1_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Maccell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthonard V., Dubin C., Castelli V., Karinka M., Vacherie B.,
 RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Crnaud C., Duprat S., Brocletier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetradodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; CA001015123; CAG13137.1; -, Genomic DNA.
 SQ SEQUENCE 2235 AA; 258437 MW; 04A0C751E04AED9 CRC64;
 Query Match 29.5%; Score 65; DB 2; Length 2235;
 Best Local Similarity 100.0%; Pred. No. 2.9e-57;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 68 DLRDGRMLIKLEVLSEGRLPKPTKGRMRHCLNVDKALQFLKEQVHLENMGSHDIVD 127
 Db 81 DLRDGRMLIKLEVLSEGRLPKPTKGRMRHCLNVDKALQFLKEQVHLENMGSHDIVD 140
 Qy 128 GNRHL 132
 Db 141 GNRHL 145
 RESULT 16
 Q90W73_gmuri

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ID 09QW73 9MURI PRELIMINARY; PRT; 332 AA.
AC 09QW73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 12, Last annotation update)
DE Beta-spectrin subunit (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10095;
RX MEDLINE=92076240; PubMed=1742606; DOI=10.1016/0361-9230(91)90066-S;
RA Zimmer W.E., Ma Y.P., Goodman S.R.;
RT "Identification of a mouse brain beta-spectrin cDNA and distribution
of its mRNA in adult tissues."
RL Brain Res. Bull. 27:187-193(1991).
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00435; Spectrin; 3.
DR SMART; SM00150; SPEC; 2.
FT NON TER 1
FT SEQUENCE 332 AA; 38192 MW; 5C9F36C840DDEEC3 CRC64;
SQ
Query Match 28.2%; Score 62; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 5.8e-55;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 RUTTELELVRRQEEERKRRPSPDPNTKYSSEAEQOMDTSGDDVSONGLPAEAGS 190
DB 204 RUTTELELVRRQEEERKRRPSPDPNTKYSSEAEQOMDTSGDDVSONGLPAEAGS 263
QY 191 PR 192
DB 264 PR 265
RESULT 17
08B035_MOUSE PRELIMINARY; PRT; 497 AA.
ID 08B035;
AC 08B035;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:DI30061A22 product:beta-spectrin 2, non-
erythrocytic, full insert sequence. (Fragment).
GN Name=Spnb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=9927925; TISSUE=spinal ganglion;
RA Carninci P., Hayashizaki Y.;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RT Meth. Enzymol. 303:19-44(1999).
[2]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=spinal ganglion;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barah G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=spinal ganglion;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[4]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=spinal ganglion;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
[5]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=spinal ganglion;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multiplexed sequencer."
RL Genome Res. 10:1757-1771(2000).
[6]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=spinal ganglion;
RC Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC 1. SIMILARITY: Contains 1 PH domain.
DR EMBL; AK051630; BAC34698.1; -; mRNA.
DR HSSP; Q62261; IBTN.
DR SMR; Q8B035; 333-438.
DR MGI; MGI:98388; Spnb2.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007182; P:common-partner SMAD protein phosphorylation; IDA.
DR GO; GO:0007184; P:SMAD protein nuclear translocation; IDA.
DR InterPro; IPR001499; PH.
DR InterPro; IPR01993; PH_type.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00169; PH; 1.

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DR Pfam; PF00435; Spectrin; 3.
DR PRINTS; SM00683; SPECTRINPH.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPEC; 2.
DR PROSITE; PS50003; PH DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 497 AA; 56537 MW; BBBA4D95709BF5F0 CRC64;

Query Match 28.2%; Score 62; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 8.6e-55;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 RLTTLELLEVRQOEERERKRRPPSPDNTKYSEAESEQMDTSKQDVSONGLPAEQGS 190
Db 212 RLTTLELLEVRQOEERERKRRPPSPDNTKYSEAESEQMDTSKQDVSONGLPAEQGS 271

Qy 191 PR 192
Db 272 PR 273

RESULT 18
08V165_RAT
ID 08V165_RAT PRELIMINARY; PRT; 66 AA.

AC 08V165;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta II spectrin-short isoform (Fragment).

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Cat T., Yu P.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF218849; AA55652.1; mRNA.

DR EMBL; ENSRN0000000543; Rattus norvegicus.

FT NON_TER 1
SQ SEQUENCE 66 AA; 7408 MW; CEAC8D69417E3B0 CRC64;

Query Match 27.3%; Score 60; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 TKVSEAESEQMDTSKQDVSONGLPAEQSPRYSQTYQYKNFNSRTTASDHSMG 219
Db 6 TKVSEAESEQMDTSKQDVSONGLPAEQSPRYSQTYQYKNFNSRTTASDHSMG 65

RESULT 19
09R1Y9_MOUSE
ID 09R1Y9_MOUSE PRELIMINARY; PRT; 48 AA.

AC 09R1Y9;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE ELF3 (Fragment).

GN Name=ELF3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Cat T., Mishra I.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF047686; AAD15747.1; Genomic_DNA.

FT NON_TER 1

FT NON_TER 48
SQ SEQUENCE 48 AA; 5393 MW; BD9CFB2CAD1632A CRC64;

Query Match 21.8%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.6e-41;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 EEBERKRRPPSPDNTKYSEAESEQMDTSKQDVSONGLPAEQSPR 192
Db 1 EEBERKRRPPSPDNTKYSEAESEQMDTSKQDVSONGLPAEQSPR 48

RESULT 20
04SR56_TETNG

ID 04SR56_TETNG PRELIMINARY; PRT; 2275 AA.

AC 04SR56;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Chromosome undetermined SCAF14494, whole genome shotgun sequence.

DE (Fragment).

ORFNames=GSTENG00013771001;

OS Tetradon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Tetraodonmura; Acanthopterygii; Perciformes; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=99883;

RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,

RA Maudet E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Daelva C., Salenoudat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Biemont C., Skalli Z., Catolico L., Poullain J., De Bernardis V.,

RA Cruaud C., Duprat S., Broctier P., Couanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Wolf J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Wincker P., Landier E.S., Weissenbach J., Roest Crollius H.;

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

the early vertebrate proto-karyotype."

RL Nature 431:946-957(2004).

RN [2]
RP NUCLEOTIDE SEQUENCE.

RG GenomeScope; Whitehead Institute Centre for Genome Research;

RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

preliminary data.

DR EMBL; CAAB01014494; CAP96656.1; Genomic_DNA.

FT NON_TER 1
SQ SEQUENCE 2275 AA; 261638 MW; 51646A21509AD94 CRC64;

Query Match 21.4%; Score 47; DB 2; Length 2275;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LPKPTKGRMRHICLENVDKALQFLKORVHLKMGSHDIVDGNHRLT 133
Db 219 LPKPTKGRMRHICLENVDKALQFLKORVHLKMGSHDIVDGNHRLT 265

RESULT 21
04SVU8_TETNG

ID 04SVU8_TETNG PRELIMINARY; PRT; 2307 AA.

AC 04SVU8;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Chromosome undetermined SCAF13839, whole genome shotgun sequence.

RT CDNA.
 RL Blood 70:915-920(1987).
 CC -1- FUNCTION: Spectrin is the major constituent of the cytoskeletal network underlying the erythrocyte plasma membrane. It associates with band 4.1 and actin to form the cytoskeletal superstructure of the erythrocyte plasma membrane.
 CC -1- SUBUNIT: Composed of nonhomologous chains, alpha and beta, which aggregate to form dimers, tetramers, and higher polymers.
 CC -1- MISCELLANEOUS: This complex is anchored to the cytoplasmic face of the plasma membrane via another protein, ankyrin, which binds to beta-spectrin and mediates the binding of the whole complex to a transmembrane protein band 3. The interaction of erythrocyte spectrin with other proteins through specific binding domains lead to the formation of an extensive subplasmalemmal meshwork which is thought to be responsible for the maintenance of the biconcave shape of human erythrocytes, for the regulation of plasma membrane components and for the maintenance of the lipid asymmetry of the plasma membrane.
 CC -1- SIMILARITY: Belongs to the spectrin family.
 CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
 CC -1- SIMILARITY: Contains 17 spectrin repeats.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 DR EMBL: S66283; AB28600.1; -; mRNA.
 DR EMBL: M18641; AAA40126.1; -; mRNA.
 DR HSSP: Q01082; 1BRK.
 DR SMR: P15508; 1055-1264.
 DR Ensembl: ENSMUSG0000021061; Mus musculus.
 DR MGI: MGI:98387; Spnbl.
 DR InterPro: IPR001589; Actinin_actin_bd.
 DR InterPro: IPR001715; Calponin_act_bd.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00307; CH; 2.
 DR Pfam: PF00435; Spectrin; 17.
 DR SMART: SM00033; CH; 2.
 DR SMART: SM00150; SPEC; 17.
 DR PROSITE: PS00019; ACTININ_1; 1.
 DR PROSITE: PS00020; ACTININ_2; 1.
 DR PROSITE: PS50021; CH; 2.
 KW Actin capping; Actin-binding; Cytoskeleton; Erythrocyte; Membrane; Repeat.
 KW Repeats.
 FT INIT MET 0
 FT DOMAIN 1 274 By similarity.
 FT DOMAIN 53 157 Actin-binding.
 FT DOMAIN 172 274 CH 1.
 FT REPEAT 275 383 CH 2.
 FT REPEAT 384 489 Spectrin 1.
 FT REPEAT 490 598 Spectrin 2.
 FT REPEAT 599 704 Spectrin 3.
 FT REPEAT 705 809 Spectrin 4.
 FT REPEAT 810 915 Spectrin 5.
 FT REPEAT 916 1022 Spectrin 6.
 FT REPEAT 1023 1129 Spectrin 7.
 FT REPEAT 1130 1235 Spectrin 8.
 FT REPEAT 1236 1340 Spectrin 9.
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 FT REPEAT 47009 47117 Spectrin 430.
 FT REPEAT 47118 47225 Spectrin 431.
 FT REPEAT 47226 47334 Spectrin 432.
 FT REPEAT 47335 47443 Spectrin 433.
 FT REPEAT 47444 47552 Spectrin 434.
 FT REPEAT 47553 47661 Spectrin 435.
 FT REPEAT 47662 47769 Spectrin 436.
 FT REPEAT 47770 47878 Spectrin 437.
 FT REPEAT 47879 47987 Spectrin 438.
 FT REPEAT 47988 48095 Spectrin 439.
 FT REPEAT 48096 48204 Spectrin 440.
 FT REPEAT 48205 48313 Spectrin 441.
 FT REPEAT 48314 48421 Spectrin 442.
 FT REPEAT 48422 48530 Spectrin 443.
 FT REPEAT 48531 48639 Spectrin 444.
 FT REPEAT 48640 48748 Spectrin 445.
 FT REPEAT 48749 48857 Spectrin 446.
 FT REPEAT 48858 48965 Spectrin 447.<

RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [8]
 RX DOMAINS:
 RA MEDLINE=84295638; PubMed=6472478;
 RA Speicher D.W., Marchesi V.T.;
 RT "Erythrocyte spectrin is comprised of many homologous triple helical
 segments.";
 RL Nature 311:177-180(1984).
 RN [9]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97001215; PubMed=8844207;
 RX DOI=10.1002/(SICI)1098-1004(1996)8:2<97::AID-HBMU1>3.3.CO;2-W;
 RA Maillet P., Allolsio N., Mople L., Delaunay J.;
 RT "Spectrin mutations in hereditary elliptocytosis and hereditary
 spherocytosis.";
 RL Hum. Mutat. 8:97-107(1996).
 RN [10]
 RP VARIANT HE CAGLIARI GLY-2017.
 RX MEDLINE=94043025; PubMed=8226774;
 RX Sahr K.E., Coetzer T.L., Moy L.S., Derick L.H., Chishti A.H.,
 RA Jacolin P., Lorenzo F., del Giudice E.M., Iolacon A., Gallanello R.,
 RA Cao A., Delaunay J., Liu S.-C., Palek J.;
 RT "Spectrin Caglieri: an Ala->Gly substitution in helix 1 of beta
 spectrin repeat 17 that severely disrupts the structure and self-
 association of the erythrocyte spectrin heterodimer.";
 RL J. Biol. Chem. 268:22656-22662(1993).
 RN [11]
 RP VARIANT HS KISSIMME ARG-201.
 RX MEDLINE=93352802; PubMed=8102379;
 RX Becker P.S., Tse W.T., Lux S.B., Forget B.G.;
 RA "Beta spectrin KISSIMME: a spectrin variant associated with autosomal
 dominant hereditary spherocytosis and defective binding to protein
 4.1.";
 RL J. Clin. Invest. 92:612-616(1993).
 RN [12]
 RP VARIANT HE PROVIDENCE PRO-2018.
 RX MEDLINE=95190014; PubMed=7883966;
 RX Gallagher P.G., Weed S.A., Tse W.T., Benoit L., Morrow J.S.,
 RA Marchesi S.L., Mohandas N., Forget B.G.;
 RT "Recurrent fetal hydrops fetalis associated with a nucleotide
 substitution in the erythrocyte beta-spectrin gene.";
 RL J. Clin. Invest. 95:1174-1182(1995).
 RN [13]
 RP VARIANTS HE VAL-2022 AND ARG-2023.
 RX MEDLINE=94289716; PubMed=8018926;
 RX Parquet N., Devaux I., Boulanger L., Galand C., Boivin P.,
 RA Lecointe M.-C., Dhermy D., Garbarz M.;
 RT "Identification of three novel spectrin alpha I/74 mutations in
 hereditary elliptocytosis: further support for a triple-stranded
 folding unit model of the spectrin heterodimer contact site.";
 RL Blood 84:303-308(1994).
 RN [14]
 RP VARIANT HE PRO-2052.
 RX MEDLINE=90369011; PubMed=1975598;
 RX Tse W.T., Lecointe M.-C., Coetsa F.F., Garbarz M., Feo C., Boivin P.,
 RA Dhermy D., Forget B.G.;
 RT "Point mutation in the beta-spectrin gene associated with alpha I/74
 hereditary elliptocytosis. Implications for the mechanism of spectrin
 dimer self-association.";
 RL J. Clin. Invest. 86:909-916(1990).
 CC -1- FUNCTION: Spectrin is the major constituent of the cytoskeletal
 network underlying the erythrocyte plasma membrane. It associates
 with band 4.1 and actin to form the cytoskeletal superstructure of
 the erythrocyte plasma membrane.
 CC -1- SUBUNIT: Composed of nonhomologous chains, alpha and beta, which
 aggregate to form dimers, tetramers, and higher polymers.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=P11277-1; Sequence=displayed;
 CC Name=2; Synonyms=Muscle-specific;
 CC IsoId=P11277-2; Sequence=VSP_000719;

CC Name=3;
 CC IsoId=P11277-3; Sequence=VSP_007242;
 CC -1- DISEASE: Defects in SPTB are a cause of rhesus-unlinked hereditary
 CC elliptocytosis (HE) (MIM:182870, 130600, 166900); also called
 CC elliptocytosis 2 (EL2). Hereditary elliptocytosis (also known as
 CC hereditary ovalocytosis) is a genetically heterogeneous, autosomal
 CC dominant hematology disorder. It is characterized by variable
 CC hemolytic anemia and elliptical or oval red cell shape. Several
 CC abnormalities in the membrane skeleton have been identified,
 CC including a number that have been localized to spectrin.
 CC Elliptocytosis due to defects in SPTB can also be referred to as
 CC elliptocytosis 3 (EL3).
 CC -1- DISEASE: Defects in SPTB are the cause of spherocytosis type I
 CC (SPT1) (MIM:182870). SPT1 is a disorder characterized by severe
 CC hemolytic anemia. Inheritance is autosomal dominant.
 CC -1- MISCELLANEOUS: This complex is anchored to the cytoplasmic face of
 CC the plasma membrane via another protein, ankyrin, which binds to
 CC beta-spectrin and mediates the binding of the whole complex to a
 CC transmembrane protein band 3. The interaction of erythrocyte
 CC spectrin with other proteins through specific binding domains lead
 CC to the formation of an extensive subplasmalemal meshwork which is
 CC thought to be responsible for the maintenance of the biconcave
 CC shape of human erythrocytes, for the regulation of plasma membrane
 CC components and for the maintenance of the lipid asymmetry of the
 CC plasma membrane.
 CC -1- SIMILARITY: Belongs to the spectrin family.
 CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
 CC -1- SIMILARITY: Contains 17 spectrin repeats.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: J05500; AAA60578.1; -; mRNA.
 CC EMBL: J05500; AAA60579.1; -; mRNA.
 CC EMBL: M37884; AAA63259.1; -; mRNA.
 CC EMBL: M37885; AAA60571.1; -; mRNA.
 CC EMBL: M57948; -; NOT ANNOTATED CDS; mRNA.
 CC EMBL: X59510; CAA42057.1; -; mRNA.
 CC EMBL: X59511; CAA42098.1; -; mRNA.
 CC EMBL: M18054; AAA60572.1; -; mRNA.
 CC PIR: A37064; STHB.
 CC PDB: 1S35; X-ray; A=1063-1274.
 CC SWISS-2DPAGE: P11277; HUMAN.
 CC Ensembl: ENSG0000070182; Homo sapiens.
 CC HGNC: HGNC:11274; SPTB.
 CC MIM: 182870; -.
 CC MIM: 130600; -.
 CC MIM: 166900; -.
 CC GO: GO:0008091; C:spectrin; TAS.
 CC GO: GO:0003779; F:actin binding; TAS.
 CC InterPro: IPR001589; Actinin_actin_bd.
 CC InterPro: IPR001715; Calponin_act_bd.
 CC InterPro: IPR02017; Spectrin.
 CC Pfam: PF00307; CH; 2.
 CC Pfam: PF00435; Spectrin; 17.
 CC SMART: SM00033; CH; 2.
 CC SMART: SM00150; SPEC; 17.
 CC PROSITE: PS00019; ACTININ_1; 1.
 CC -----
 CC Query Match 17.3%; Score 38; DB 1; Length 2136;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-29;
 CC Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 95 MRHCLENVKALQFLKEORVHLENGSHDIYDGNHRL 132
 CC |||||
 CC Db 107 MRHCLENVKALQFLKEORVHLENGSHDIYDGNHRL 144
 CC -----
 CC RESULT 25
 CC Q6XDAO_RAT

RT isoforms of beta1 spectrin have distinct intracellular locations and activities."

RL J. Cell Sci. 113:2023-2034(2000).

DR EMBL; AJ242018; CAB42616.1; -, mRNA.

DR RGD; 621726; Spnbl.

FT NON_TER 1

SQ SEQUENCE 82 AA; 9526 MW; 6FDA86568647C6E9 CRC64;

Query Match 16.8%; Score 37; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 9.9e-30;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 OVSQNGLPAAQSGSPRVSYRQTYQNYKNFNSRTASD 214

DB 40 OVSQNGLPAAQSGSPRVSYRQTYQNYKNFNSRTASD 76

RESULT 29

QSD002_RAT PRELIMINARY; PRT; 516 AA.

AC QSD002;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Spnbl protein (Fragment).

GN Name=Spnbl2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxId=10116;

NP NUCLEOTIDE SEQUENCE.

RA MEDLINE=22388237; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaller G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F., Dietzchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stjepeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.D., Utsch T.B., Toshiyuki S., Carninci P., Pange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE-Ovary;

RG NIH MGC Project;

RL Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Contains 1 PH domain.

DR EMBL; BC090340; AAH90340.1; -, mRNA.

DR SMR; QSD002; 352-457.

DR InterPro; IPR001849; PH.

DR InterPro; IPR002017; Spectrin.

DR InterPro; IPR001605; Spectrin_PH.

DR Pfam; PF00169; PH; 1.

DR Pfam; PF00435; Spectrin; 2.

DR PRINTS; PR00683; SPECTRINPH.

DR SMART; SM00233; PH; 1.

DR SMART; SM00150; SPEC; 2.

DR PROSITE; PS50003; PH_DOMAIN; 1.

FT NON_TER 1

SQ SEQUENCE 516 AA; 58595 MW; 2969B75C89F71A3A CRC64;

Query Match 14.5%; Score 32; DB 2; Length 516;

Best Local Similarity 100.0%; Pred. No. 8.6e-24;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KYSEEAESQWDTSKGDQVQNGLPAAQSGSPR 192

DB 261 KYSEEAESQWDTSKGDQVQNGLPAAQSGSPR 292

RESULT 30

Q4SF10_TETNG PRELIMINARY; PRT; 2413 AA.

AC Q4SF10;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Chromosome 7 SCAP14601, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG00019086001;

OS Tetradodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

NCBI_TaxId=99863;

NP NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozou-Costaz C., Bernot A., Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard C., Rubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cateolico L., Poulain J., De Bernardinis V., Cruaud C., Duprat S., Broctier P., Coutancan J.P., Gonzy J., Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S., Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Queller F., Sautin W., Scarpelli C., Winkler P., Lander E.S., Weissbach J., Roest Crolious H., "Genome duplication in the teleost fish Tetradodon nigroviridis reveals the early vertebrate proto-karyotype."

RL Nature 431:946-957(2004).

RP NUCLEOTIDE SEQUENCE.

RG Genoscope, Whitehead Institute Centre for Genome Research;

RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).

CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).

CC -1- SIMILARITY: Contains 1 PH domain.

DR EMBL; CA601014601; CAG00602.1; -, Genomic DNA.

DR InterPro; IPR001589; Actinin_actin_bd.

DR InterPro; IPR001715; Actinin_act_bd.

DR InterPro; IPR001849; PH.

DR InterPro; IPR002017; Spectrin.

DR InterPro; IPR001605; Spectrin_PH.

DR Pfam; PF00307; CH; 2.

DR Pfam; PF00169; PH; 1.

DR Pfam; PF00435; Spectrin; 17.

DR PRINTS; PR00683; SPECTRINPH.

DR SMART; SM00233; CH; 2.

DR SMART; SM00150; SPEC; 17.

DR PROSITE; PS00019; ACTININ_1; 1.

DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS50003; PH DOMAIN; 1.
FT NON TER 1
SQ SEQUENCE 2413 AA; 277305 MW; 8EA3A927A2C17FBB CRC64;
Query Match 12.7%; Score 28; DB 2; Length 2413;
Best Local Similarity 100.0%; Pred. No. 5.2e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 LEGRFQLODEREAVOKTFTKVNSHL 55
DB 79 LEGRFQLODEREAVOKTFTKVNSHL 106
RESULT 31
O5XG36_XENLA PRELIMINARY; PRT; 794 AA.
AC O5XG36;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE LOC398511 protein (fragment).
GN Name=LOC398511;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=83355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094634; AA04634.1; -, mRNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind_actin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; CH; 2.

DR Pfam; PF00435; Spectrin; 5.
DR SMART; SM00033; CH; 2.
DR SMART; SM00150; SPEC; 4.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
FT NON TER 794
SQ SEQUENCE 794 AA; 92657 MW; 96F2259167965456 CRC64;
Query Match 12.3%; Score 27; DB 2; Length 794;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 87 LPKPTKGRMRHICLENVDKALQFLKEQ 113
DB 103 LPKPTKGRMRHICLENVDKALQFLKEQ 129
RESULT 32
O7ZX11_XENLA PRELIMINARY; PRT; 1060 AA.
AC O7ZX11;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE LOC398511 protein (fragment).
GN Name=LOC398511;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=83355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046267; AA046267.1; -, mRNA.
DR HSP; 001082; IBKR.
DR GO; GO:0003779; F:actin binding; IEA.

```

DR InterPro: IPR001589; Actbind actin.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR002017; Spectrin.
DR Pfam: PF00307; CH_2.
DR Pfam: PF00435; Spectrin; 7.
DR SMART: SM00033; CH_2.
DR SMART: SM00150; SPEC; 7.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PS00020; ACTININ_2; 1.
DR PROSITE: PS50021; CH_2.
DR NON_TER 1060 1060
SQ SEQUENCE 1060 AA; 122756 MW; ABD56DC56C4CAl1B CRC64;

Query Match 12.3%; Score 27; DB 2; Length 1060;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 87 LPKPTGRMRTHCLENVKALQFLKEQ 113
Db 103 LPKPTGRMRTHCLENVKALQFLKEQ 129

RESULT 33
SPTN2 RAT STANDARD; PRT; 2388 AA.
AC Q9QMN2; O88197; O9SE68;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Spectrin beta chain, brain 2 (Spectrin, non-erythroid beta chain 2)
DE (Beta-III spectrin) (SPMB-3) (Beta SpIII sigma 1) (Spectrin-like
DE protein GRBPp11).
GN Name=SpChn2;
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96340016; PubMed=9675416; DOI=10.1016/S0169-328X(98)00068-0;
RX Chara O., Chara R., Yamakawa H., Nakajima D., Nakayama M.;
RT "Characterization of a new beta-spectrin gene which is predominantly
RT expressed in brain.";
RL Brain Res. Mol. Brain Res. 57:181-192(1998).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=9639639; PubMed=9704016; DOI=10.1006/dbrc.1998.9067;
RX Sakaguchi G., Orita S., Naito A., Maeda M., Igaraishi H., Sasaki T.,
RX Takai Y.;
RT "A novel brain-specific isoform of beta spectrin: isolation and its
RT interaction with Munc13.";
RL Biochem. Biophys. Res. Commun. 248:846-851(1998).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC Rothstein J.D., Jackson M.;
RT "GRAP1- a cytoskeletal modulator of EAAT4 glutamate transporter.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably plays an important role in neuronal membrane
CC skeleton.
CC -1- TISSUE SPECIFICITY: Abundantly transcribed in the brain. Neurons
CC are the predominant cell-type to express the gene. Found
CC abundantly in Purkinje cells.
CC -1- SIMILARITY: Belongs to the spectrin family.
CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 17 spectrin repeats.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB008551; BAA32699.1; -; mRNA.
DR EMBL; AB001347; BAA32473.1; -; mRNA.
DR EMBL; AF225960; AAC28596.1; -; mRNA.
DR PIR; JEO271; JEO271.
DR HSSP; Q01082; 1BRK.
DR SMK; Q9QMN8; 2212-2333.
DR Ensembl; ENSRNOG00000019564; Rattus norvegicus.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0016363; C:nuclear matrix; TAS.
DR GO; GO:0008091; C:spectrin; TAS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR GO; GO:0017158; P:regulation of calcium ion-dependent exocytosis; TAS.
DR GO; GO:0016081; P:synaptic vesicle docking during exocytosis; TAS.
DR InterPro; IPR001589; Actinin actin bd.
DR InterPro; IPR001715; Calponin_act_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00435; Spectrin_17.
DR PRINTS; P000683; SPECTRINPH.
DR SMART; SM00033; CH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPEC; 17.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR Actin capping; Actin-binding; Cytoskeleton; Membrane; Repeat.
DR DOMAIN 1 278
FT DOMAIN 57 161 CH 1.
FT DOMAIN 176 278 CH 2.
FT REPEAT 305 415 Spectrin 1.
FT REPEAT 425 529 Spectrin 2.
FT REPEAT 531 639 Spectrin 3.
FT REPEAT 641 745 Spectrin 4.
FT REPEAT 747 850 Spectrin 5.
FT REPEAT 852 956 Spectrin 6.
FT REPEAT 958 1063 Spectrin 7.
FT REPEAT 1065 1170 Spectrin 8.
FT REPEAT 1172 1276 Spectrin 9.
FT REPEAT 1278 1381 Spectrin 10.
FT REPEAT 1383 1486 Spectrin 11.
FT REPEAT 1488 1586 Spectrin 12.
FT REPEAT 1588 1692 Spectrin 13.
FT REPEAT 1694 1799 Spectrin 14.
FT REPEAT 1801 1905 Spectrin 15.
FT REPEAT 1907 2011 Spectrin 16.
FT REPEAT 2013 2075 Spectrin 17.
FT DOMAIN 2218 2328 PH.
FT DOMAIN 326 328 VTL -> GTF (in Ref. 3).
FT CONFILCT 543 543 L -> F (in Ref. 2).
FT CONFILCT 608 608 D -> G (in Ref. 3).
FT CONFILCT 887 887 L -> P (in Ref. 3).
FT CONFILCT 908 908 V -> I (in Ref. 3).
FT CONFILCT 948 948 D -> G (in Ref. 3).
FT CONFILCT 1156 1157 BL -> GA (in Ref. 2).
FT CONFILCT 1194 1194 F -> V (in Ref. 2 and 3).
FT CONFILCT 1555 1555 G -> R (in Ref. 3).
FT CONFILCT 1769 1769 R -> W (in Ref. 3).
SO SEQUENCE 2388 AA; 271064 MW; 3EC8966AF065F19 CRC64;

Query Match 12.3%; Score 27; DB 1; Length 2388;
Best Local Similarity 100.0%; Pred. No. 5,5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 103 LPKPTKGRMRHICLENVDKALQFLKEQ 129

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RESULT 34
ID 068FG2_MOUSE PRELIMINARY; PRT; 2388 AA.
AC 068FG2;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28; last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, last annotation update)
DE Spectrin beta 3.
GN Name=Spm3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; BC079860; AAH79860.1; -, mRNA.
DR SMR; 068FG2; 2212-2333.
DR Ensemble; ENSMUSG0000067889; Mus musculus.
DR MGI; MGI:1313261; Spm3.
DR GO; GO:0003779; F-actin binding; IEA.
DR InterPro; IPR001589; Actinin actin bd.
DR InterPro; IPR001715; Calponin_act_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR02017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00435; PH; 1.
DR Pfam; PF00435; Spectrin; 17.
DR PRINTS; PRO0663; SPECTRINPH.
DR SMART; SM00033; CH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPM; 17.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR Actin capng; Actin-binding; Cytoskeleton.
SO SEQUENCE 2388 AA; 270923 MW; 19DA7460B75576D1 CRC64;
Query Match 12.3%; Score 27; DB 2; Length 2388;

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Best Local Similarity 100.0%; Pred. No. 5,5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LPKPTKGRMRHICLENVDKALQFLKEQ 113
Db 103 LPKPTKGRMRHICLENVDKALQFLKEQ 129

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RESULT 35
SPTN2_HUMAN STANDARD; PRT; 2390 AA.
ID SPTN2_HUMAN
AC 015020; 014872; 014873;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 10-MAY-2005 (Rel. 47, last annotation update)
DE Spectrin beta chain, brain 2 (Spectrin, non-erythroid beta chain 2)
DE (beta-III spectrin).
GN Name=SPTN2; Synonyms=XRMA0302;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=9734984; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL DNA Res. 4:141-150 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1-34.
RC TISSUE=Brain;
RX MEDLINE=9904654; PubMed=9826670; DOI=10.1073/pnas.95.24.14158;
RA Stankewich M.C., Tee W.T., Peters L.L., Chng Y., John K.M.,
RA Stach P.R., Devarejan P., Morrow J.S., Lux S.E.;
RT "A widely expressed betaactin spectrin associated with Golgi and
RT cytoplasmic vesicles."
RT Proc. Natl. Acad. Sci. U.S.A. 95:14158-14163 (1998).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1900-2390 (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RA Tee W.T., Peters L.L., John K.M., Lux S.E.;
RT "SPTN2, a new, widely expressed beta III spectrin gene located on
RT human chromosome 11q13 and mouse chromosome 19."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably plays an important role in neuronal membrane
CC skeleton.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=2;
CC Name=1;
CC IsoId=015020-1; Sequence=Displayed;
CC Name=2;
CC IsoId=015020-2; Sequence=VSP_000722;
CC -1- TISSUE SPECIFICITY: Highly expressed in brain, kidney, pancreas,
CC and liver, and at lower levels in lung and placenta.
CC -1- SIMILARITY: Belongs to the spectrin family.
CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 17 spectrin repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB008567; BAA22700.1; -, mRNA.
CC DR EMBL; AF079569; AAC80006.1; -, mRNA.
CC EMBL; AF026487; AAC79502.1; -, mRNA.

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DR EMBL: AF026488; AAC79503.1; -; mRNA.
DR EMBL: AF026488; AAC79504.1; -; mRNA.
DR PDB: 1WJM; NMR; A=2219-2326.
DR SMR: O15020; 2212-2333.
DR Eneemb1; ENSG00000173898; Homo sapiens.
DR H-InvDB; HGNC:11276; SPTBN2.
DR MIM; 604965; -.
DR GO; GO:0030138; C:COPII-coated vesicle; TAS.
DR GO; GO:0008091; C:spectrin; IEA.
DR GO; GO:0003779; F:actin binding; TAS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR GO; GO:0016192; F:vesicle-mediated transport; IDA.
DR InterPro; IPR001589; Actinin actin bd.
DR InterPro; IPR001715; Calponin_act_bd.
DR InterPro; IPR001649; PH.
DR InterPro; IPR011993; PH_type.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00435; Spectrin; 17.
DR PRINTS; PR00683; SPECTRINPH.
DR SMART; SM00033; CH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPEC; 17.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR 3D-structure; Actin capping; Actin-binding; Alternative splicing;
KW Cytoskeleton; Membrane; Repeat.
FT DOMAIN 1 278 Actin-binding (By similarity).
FT DOMAIN 57 161 CH 1.
FT DOMAIN 176 278 CH 2.
FT REPEAT 305 415 Spectrin 1.
FT REPEAT 425 529 Spectrin 2.
FT REPEAT 531 639 Spectrin 3.
FT REPEAT 641 745 Spectrin 4.
FT REPEAT 747 850 Spectrin 5.
FT REPEAT 852 956 Spectrin 6.
FT REPEAT 958 1063 Spectrin 7.
FT REPEAT 1065 1170 Spectrin 8.
FT REPEAT 1172 1276 Spectrin 9.
FT REPEAT 1278 1381 Spectrin 10.
FT REPEAT 1383 1486 Spectrin 11.
FT REPEAT 1488 1586 Spectrin 12.
FT REPEAT 1588 1692 Spectrin 13.
FT REPEAT 1694 1799 Spectrin 14.
FT REPEAT 1801 1905 Spectrin 15.
FT REPEAT 1907 2011 Spectrin 16.
FT REPEAT 2013 2075 Spectrin 17.
FT DOMAIN 2218 2330 PH.
FT VARSPLIC 2314 2390
AEMSSMLRVNNAIAITASSASGEPEPVVPTTRGQTRAMT
MPVPSVGAEGPVLRKSGRERERKSPFKOKK -> V
SCPSCSLSVPRQKLPAADSPSPVLPJLPGVLGKTKGCV
RRPHQALPV (in isoform 2).
/FTID=VSP_000722.
SQ SEQUENCE 2390 AA; 271295 MW; E8C3033DD25A674C CRC64;

Query Match 12.3%; Score 27; DB 1; Length 2390;
Best Local Similarity 100.0%; Pred. No. 5.5e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS Beta-spectrin (Fragment).
GN Name=HSP7B1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RX MEDLINE=9811272; PubMed=9450796;
RX DOI=10.1046/j.1365-2141.1998.00530.x;
RA Garbarr M., Galand C., Bibes D., Bournier O., Devaux I.,
RA Haroussau J.L., Grandchamp B., Dhery D.,
RT "A 5' splice region G->C mutation in exon 3 of the human beta-
RT spectrin gene leads to decreased levels of beta-spectrin mRNA and is
RT responsible for dominant hereditary spherocytosis (spectrin Guemene-
RT Penfao).";
RL Br. J. Haematol. 100:90-98(1998).
DR EMBL: AF013172; AAC02786.1; -; Genomic_DNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS50021; CH; 1.
FT NON_TER 1 1
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 6035 MW; 29F9A04CD7A8031 CRC64;

Query Match 11.4%; Score 25; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 36
Q71VG2 HUMAN
ID Q71VG2 HUMAN PRELIMINARY; PRT; 51 AA.
AC Q71VG2;

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Qy 42 VQKFTKVNSHARVSCRITDLY 66
Db 6 VQKFTKVNSHARVSCRITDLY 30

RESULT 37
Q71S06 HUMAN
ID Q71S06 HUMAN PRELIMINARY; PRT; 2002 AA.
AC Q71S06;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS Beta Spectrin IV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yu P., Chen Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324064; AAQ14859.1; -; mRNA.
DR HSSP; Q01082; 1AA2.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00435; Spectrin; 16.
DR SMART; SM00033; CH; 2.
DR SMART; SM00150; SPEC; 14.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
SQ SEQUENCE 2002 AA; 225564 MW; 627B9616D192AE30 CRC64;

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Query Match 10.0%; Score 22; DB 2; Length 2002;
 Best Local Similarity 100.0%; Pred. No. 6.6e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 DEREAVOKKFTTKVNSHARV 58
 |||||
 Db 57 DEREAVOKKFTTKVNSHARV 78
 |||||

RESULT 38
 Q912E6 MOUSE PRELIMINARY; PRT; 2555 AA.
 AC Q912E6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Beta4-spectrin (Beta-spectrin 4).
 GN Name=Spnb4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21419653; PubMed=11528393; DOI=10.1038/ng710;
 RA Parkinson N.J., Olsson C.L., Hallows J.L., McKee-Johnson J.,
 RA Keogh B.P., Noben-Trauth K., Kujawa S.G., Tempel B.L.;
 RT "Mutant beta-spectrin 4 causes auditory and motor neuropathies in
 RT quivering mice".
 RL Nat. Genet. 29:61-65(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Parkinson N.J., Olsson C.L., Hallows J.L., Kujawa S.G.,
 RA McKee-Johnson J., Noben-Trauth K., Keogh B.P., Tempel B.L.;
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AY032720; AAK49014.1; -; Genomic DNA.
 DR EMBL; AY032655; AAK38731.1; -; mRNA.
 DR EMBL; AY032702; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032700; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032698; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032694; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032696; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032693; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032697; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032701; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032708; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032709; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032710; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032711; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032712; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032713; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032714; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032705; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032703; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032704; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032715; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032716; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032717; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032718; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032719; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032706; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032707; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032699; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032695; AAK49014.1; JOINED; Genomic DNA.
 DR EMBL; AY032692; AAK49014.1; JOINED; Genomic DNA.
 DR HSSP; C01082; 1BKR.
 DR MGI; MGI:1890574; Spnb4.
 DR GO; GO:0030424; C:axon; IDA.
 DR GO; GO:0043203; C:axon hillock; IDA.

DR GO; GO:0005737; C:cytoplasm; ISS.
 DR GO; GO:0016363; C:nuclear matrix; ISS.
 DR GO; GO:0016605; C:PM body; ISS.
 DR GO; GO:0008091; C:spectrin; ISS.
 DR GO; GO:0003779; F:actin binding; ISS.
 DR GO; GO:0030506; F:ankyrin binding; ISS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
 DR GO; GO:0007016; P:cytoskeletal anchoring; ISS.
 DR GO; GO:0007605; P:perception of sound; IMP.
 DR GO; GO:0019226; P:transmission of nerve impulse; IMP.
 DR GO; GO:0016192; P:vesicle-mediated transport; ISS.
 DR InterPro; IPR001589; Actin actin bd.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR InterPro; IPR011993; PH_type.
 DR InterPro; IPR002017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00435; Spectrin; 17.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00150; SPEC; 16.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR Actin capring; Actin-binding; Cytoskeleton.
 DR SEQUENCE 2555 AA; 288135 MW; 39FEC7E410289D45 CRC64;

Query Match 10.0%; Score 22; DB 2; Length 2555;
 Best Local Similarity 100.0%; Pred. No. 8.6e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 DEREAVOKKFTTKVNSHARV 58
 |||||
 Db 58 DEREAVOKKFTTKVNSHARV 79
 |||||

RESULT 39
 Q912E6 MOUSE PRELIMINARY; PRT; 2561 AA.
 AC Q912E6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Beta4-spectrin signal.
 GN Name=Spnb4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21666188; PubMed=11807096; DOI=10.1083/jcb.200110003;
 RA Komada M., Soriano P.;
 RT "[beta]4-spectrin regulates sodium channel clustering through
 RT ankyrin-G at axon initial segments and nodes of Ranvier.";
 RL J. Cell Biol. 156:337-348(2002).
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AB055618; BAB83243.1; -; mRNA.
 DR HSSP; C01082; 1BKR.
 DR MGI; MGI:1890574; Spnb4.
 DR GO; GO:0030424; C:axon; IDA.
 DR GO; GO:0043203; C:axon hillock; IDA.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0016363; C:nuclear matrix; IDA.
 DR GO; GO:0007605; P:perception of sound; IMP.
 DR GO; GO:0019226; P:transmission of nerve impulse; IMP.
 DR InterPro; IPR001589; Actin actin bd.
 DR InterPro; IPR001715; Calponin_act_bd.

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DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00307; CH 2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00435; Spectrin; 17.
DR PRINTS; PR00683; SPECTRINPH.
DR SMART; SM00033; CH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPC; 16.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS50003; PH DOMAIN; 1.
KW Actin capping; Actin-binding; Cytoskeleton.
SQ SEQUENCE 2561 AA; 288809 MW; 4DF01A9180140F33 CRC64;

Query Match 10.0%; Score 22; DB 2; Length 2561;
Best Local Similarity 100.0%; Pred.No. 8.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 DEREAOKKTFKWNSHARV 58
Db 58 DEREAOKKTFKWNSHARV 79

RESULT 40
SPFN4_HUMAN STANDARD; PRT; 2564 AA.
ID SPFN4_HUMAN
AC Q9H254; Q9H1K7; Q9H1K8; Q9H1K9; Q9H3G8; Q9HCD0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain 3)
DE (Beta-IV spectrin).
GN Name=SPFN4; Synonyms=KTA1642, SPTBN3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo;
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=21316449; PubMed=11294830; DOI=10.1074/jbc.M009307200;
RA Tse W.T., Tang J., Jin O., Korogren C., John K.M., Kung A.L.,
RA Gwynn B., Peters J.L., Lux S.E.;
RT "A new spectrin, beta-IV, has a major truncated isoform that
RT associates with promyelocytic leukemia protein nuclear bodies and the
RT nuclear matrix."
RT J. Biol. Chem. 276:23974-23985(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RX MEDLINE=20539976; PubMed=11086001; DOI=10.1083/jcb.151.5.985;
RA Berghs S., Aggujaro D., Ditz R. Jr., Maksimova E., Stabach P.,
RA Hermler J.-M., Zhang J.-P., Philbrick W., Slepnev V., Ort T.,
RA Solimena M.;
RT "BetaIV spectrin, a new spectrin localized at axon initial segments
RT and nodes of Ranvier in the central and peripheral nervous system."
RT J. Cell Biol. 151:985-1002(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 386-2382 (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro."
RL DNA Res. 7:273-281(2000).
CC -1- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H254-1; Sequence=Displayed;

```

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CC Name=2;
CC IsoId=Q9H254-2; Sequence=VSP_000725, VSP_000726;
CC Name=3;
CC IsoId=Q9H254-3; Sequence=VSP_000723, VSP_000724;
CC Name=4;
CC IsoId=Q9H254-4; Sequence=VSP_000727, VSP_000728;
CC -1- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic
CC islets.
CC -1- SIMILARITY: Belongs to the spectrin family.
CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 18 spectrin repeats.
CC -----
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CC use as long as its content is in no way modified and this statement is not
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CC -----
CC EMBL; AF311855; AAG42473.1; -; mRNA.
CC EMBL; AF082075; AAG38874.1; -; mRNA.
CC EMBL; AY004226; AAF93171.1; -; mRNA.
CC EMBL; AY004226; AAF93172.1; -; mRNA.
CC EMBL; AY004227; AAF93173.1; -; mRNA.
CC EMBL; AB046862; BAB13468.1; -; mRNA.
CC HSSP; Q01082; 1BKR.
CC Ensembl; ENSG00000160460; Homo sapiens.
CC HGN; HGNC:14896; SPTBN4.
CC MIM; 606214; -;
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0016363; C:nuclear matrix; IDA.
CC GO; GO:0016505; C:PMI body; IDA.
CC GO; GO:0008093; C:spectrin; IDA.
CC GO; GO:0003779; F:actin binding; TAS.
CC GO; GO:0030506; F:ankyrin binding; IDA.
CC GO; GO:0005200; P:structural constituent of cytoskeleton; TAS.
CC GO; GO:0007016; P:cytoskeletal anchoring; TAS.
CC GO; GO:0016192; P:vesicle-mediated transport; TAS.
CC InterPro; IPR001589; Actinin actin bd.
CC InterPro; IPR001715; Calponin_act_bd.
CC InterPro; IPR001849; PH.
CC InterPro; IPR011993; PH type.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR001605; Spectrin_PH.
CC Pfam; PF00307; CH; 2.
CC Pfam; PF00169; PH; 1.
CC PRINTS; PR00683; SPECTRINPH.
CC SMART; SM00033; CH; 2.
CC SMART; SM00233; PH; 1.
CC SMART; SM00150; SPC; 16.
CC PROSITE; PS00019; ACTININ_1; 1.
CC PROSITE; PS00020; ACTININ_2; 1.
CC PROSITE; PS50021; CH; 2.
CC PROSITE; PS50003; PH DOMAIN; 1.
KW Actin capping; Actin-binding; Alternative splicing; Cytoskeleton;
KW Membrane; Repeat.
FT DOMAIN 1 282 Actin-binding (By similarity).
FT DOMAIN 61 165 CH 1.
FT DOMAIN 180 282 CH 2.
FT REPEAT 309 354 Spectrin 1.
FT REPEAT 398 419 Spectrin 2.
FT REPEAT 429 533 Spectrin 3.
FT REPEAT 535 642 Spectrin 4.
FT REPEAT 644 771 Spectrin 5.
FT REPEAT 773 879 Spectrin 6.
FT REPEAT 881 985 Spectrin 7.
FT REPEAT 1019 1086 Spectrin 8.
FT REPEAT 1199 1303 Spectrin 9.
FT REPEAT 1305 1408 Spectrin 10.
FT REPEAT 1410 1513 Spectrin 11.
FT REPEAT 1515 1619 Spectrin 12.
FT REPEAT 1515 1619 Spectrin 13.

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FT REPEAT 1621 1725 Spectrin 14.
FT REPEAT 1727 1832 Spectrin 15.
FT REPEAT 1834 1940 Spectrin 16.
FT REPEAT 1942 2046 Spectrin 17.
FT REPEAT 2048 2107 Spectrin 18.
FT DOMAIN 2418 2527 PH.
FT VARSPLIC 1 1257 Missing (in isoform 3).
FT VARSPLIC 1258 1286 /FTId=VSP_000723.
FT VARSPLIC 1287 1309 AVOAAGLRCGNYEGQAQAVRLLEK -> MPHYPSCS
FT VARSPLIC 1309 /FTId=VSP_000724.
FT VARSPLIC 1310 2564 NOENOLRAQOMWOKLHDLQOH -> CLIHPLALHPWE
FT VARSPLIC 2113 2154 PLYLPRSSS (in isoform 2).
FT VARSPLIC 2113 2154 /FTId=VSP_000725.
FT VARSPLIC 2155 2564 Missing (in isoform 2).
FT VARSPLIC 2155 2564 /FTId=VSP_000726.
FT CONFLICT 604 608 /FTId=VSP_000728.
FT CONFLICT 714 714 Missing (in Ref. 2).
FT CONFLICT 1189 1189 L -> S (in Ref. 2).
FT CONFLICT 1193 1193 E -> K (in Ref. 2).
FT CONFLICT 1331 1331 G -> S (in Ref. 1).
SQ SEQUENCE 2564 AA; 288985 MW; 52CDE7D1DB01BCC CRC64;

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Query Match 10.0%; Score 22; DB 1; Length 2564;
Best Local Similarity 100.0%; Pred. No. 8.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 37 DEREAVOKTFTKWNHSHLAV 58
Db 57 DEREAVOKTFTKWNHSHLAV 78

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RESULT 41
ID Q71S07 HUMAN PRELIMINARY; PRT; 2564 AA.
AC Q71S07;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Non-erythrocytic beta-spectrin 4.
GN Name=SPN84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Cal T.;
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AF324063; AAQ14860.1; -; mRNA.
DR HSSP; Q01082; 1AA2.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actinin actin bd.
DR InterPro; IPR001715; Calponin act_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00683; SPECTRINPH.
DR SMART; SM00033; CH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPEC; 16.
DR PROSITE; PS00019; ACTININ_1; 1.

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DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS50023; PH DOMAIN; 1.
KW Actin capping; Actin-binding; Cytoskeleton.
SQ SEQUENCE 2564 AA; 289061 MW; CB1CACB2FF97776 CRC64;

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Query Match 10.0%; Score 22; DB 2; Length 2564;
Best Local Similarity 100.0%; Pred. No. 8.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 37 DEREAVOKTFTKWNHSHLAV 58
Db 57 DEREAVOKTFTKWNHSHLAV 78

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RESULT 42
ID Q6NNX2 DROME PRELIMINARY; PRT; 1410 AA.
AC Q6NNX2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE A12441p (Fragment).
DE Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN NCBI_TaxID=7227;
RN NUCLEOTIDE SEQUENCE.
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Murgall C.J., Nunoo J., Pacleb J., Patagas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Cealiker S.;
RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; BT011160; AAR82828.1; -; mRNA.
DR HSSP; Q01082; 1AA2.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind actinin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00435; Spectrin; 10.
DR SMART; SM00033; CH; 2.
DR SMART; SM00150; SPEC; 10.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
FT NON TER 1410 1410
SQ SEQUENCE 1410 AA; 164827 MW; 3346E537C78AA48B CRC64;

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Query Match 8.6%; Score 19; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 75 LKLEVLVSGERLPKPTKG 93
Db 84 LKLEVLVSGERLPKPTKG 102

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RESULT 43
ID SPTCB DROME STANDARD; PRT; 2291 AA.
AC Q00963; Q9VX30;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Spectrin beta chain.
GN Name=beta-Spec; Synonyms=Spec-b; ORFNames=CG5870;
OS Drosophila melanogaster (Fruit fly).

```

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=92335263; PubMed=1631106;
 RA Byers T.J., Brandon B., Lue R., Winograd E., Branton D.,
 RT "The complete sequence of Drosophila beta-spectrin reveals supra-
 RT motifs comprising eight 106-residue segments."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6187-6191(1992).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayant A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Duthin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Horin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasero P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskeas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weltschbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochink S.E.,
 RA Smith C.D., Tupy J.D., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [4]
 RP CHARACTERIZATION.
 RX MEDLINE=88059242; PubMed=3680372; DOI=10.1083/jcb.105.5.2095;
 RA Dubreuil R., Byers T.J., Branton D., Goldstein L.S.B., Kiehart D.P.,
 RT "Drosophila spectrin. I. Characterization of the purified protein."
 RL J. Cell Biol. 105:2095-2102(1987).
 [5]

RP STRUCTURE BY NMR OF 2145-2262.
 RX MEDLINE=96164435; PubMed=8591029; DOI=10.1016/S0969-2126(01)00254-4;
 RA Zhang P., Talluri S., Deng H., Branton D., Wagner G.,
 RT "Solution structure of the pleckstrin homology domain of Drosophila
 RT beta-spectrin."
 RL Structure 3:1185-1195(1995).
 CC -1- FUNCTION: Spectrin is the major constituent of the cytoskeletal
 CC network underlying the erythrocyte plasma membrane. It associates
 CC with band 4.1 and actin to form the cytoskeletal superstructure of
 CC the erythrocyte plasma membrane. Interacts with calmodulin in a
 CC calcium-dependent manner.
 CC -1- SUBUNIT: Native spectrin molecule is a tetramer composed of two
 CC antiparallel heterodimers joined head to head so that each end of
 CC the native molecule includes the C-terminus of the alpha subunit
 CC and the N-terminus of the beta subunit.
 CC -1- INTERACTION:
 CC Q9YTA2:CGI0627; Ndxp21; Intact=EBI-75025, EBI-119881;
 CC -1- SIMILARITY: Belongs to the spectrin family.
 CC -1- SIMILARITY: Contains 2 CH (calponin-homology) domains.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 17 spectrin repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; M92288; AAA28399.1; -, mRNA.
 CC EMBL; AE003506; AAF48751.1; -, Genomic DNA.
 CC PIR; A46147; A46147.
 CC PDB; 1DRO; NMR; @2145-2262.
 CC Intact; Q00963; -;
 CC Ensembl; CG5870; Drosophila melanogaster.
 CC Flybase; FBgn0003471; Beta-Spec.
 CC GO; GO:0016327; C:apicolateral plasma membrane; TAS.
 CC GO; GO:0045169; C:fusome; IDA.
 CC GO; GO:0045170; C:spectrosome; IDA.
 CC GO; GO:0008017; P:microtubule binding; IDA.
 CC GO; GO:0045478; P:fusome organization and biogenesis; TAS.
 CC GO; GO:0007274; P:neuromuscular synaptic transmission; IMP.
 CC GO; GO:0007009; P:plasma membrane organization and biogenesis; TAS.
 CC GO; GO:0030721; P:spectrosome organization and biogenesis; TAS.
 CC InterPro; IPR001589; Actinin actin bd.
 CC InterPro; IPR001715; Calponin_act_bd.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR011993; PH type.
 CC InterPro; IPR002017; Spectrin.
 CC InterPro; IPR001605; Spectrin_PH.
 CC Pfam; PF00307; CH; 2.
 CC Pfam; PF00169; PH; 1.
 CC Pfam; PF00435; Spectrin; 17.
 CC PRINTS; PR00683; SPECTRINPH.
 CC SMART; SMO0033; CH; 2.
 CC SMART; SMO0233; PH; 1.
 CC SMART; SMO0150; SPEC; 17.
 CC PROSITE; PS00019; ACTININ_1; 1.
 CC PROSITE; PS00021; CH; 2.
 CC PROSITE; PS00020; ACTININ_2; 1.
 CC PROSITE; PS50003; PH DOMAIN; 1.
 CC 3D-structure; Actin-binding; Actin-binding; Calmodulin-binding;
 CC Cytoskeleton; Membrane; Repeat.
 CC DOMAIN 1 271 Actin-binding (By similarity).
 CC FT DOMAIN 50 154 CH 1.
 CC FT DOMAIN 169 271 CH 2.
 CC FT REPEAT 298 408 Spectrin 1.
 CC FT REPEAT 418 522 Spectrin 2.
 CC FT REPEAT 524 633 Spectrin 3.
 CC FT REPEAT 635 739 Spectrin 4.
 CC FT REPEAT 741 844 Spectrin 5.
 CC FT REPEAT 846 950 Spectrin 6.
 CC FT REPEAT 952 1057 Spectrin 7.
 CC FT REPEAT 1059 1167 Spectrin 8.

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FT REPEAT 1169 1273 Spectrin 9.
FT REPEAT 1275 1378 Spectrin 10.
FT REPEAT 1380 1485 Spectrin 11.
FT REPEAT 1487 1591 Spectrin 12.
FT REPEAT 1593 1697 Spectrin 13.
FT REPEAT 1699 1804 Spectrin 14.
FT REPEAT 1806 1910 Spectrin 15.
FT REPEAT 1912 2016 Spectrin 16.
FT REPEAT 2018 2078 Spectrin 17.
FT DOMAIN 2147 2259 PH.
FT CONFLICT 2278 2278 D -> Y (in Ref. 1).
FT STRAND 2150 2157
FT TURN 2166 2167
FT STRAND 2173 2179
FT STRAND 2185 2187
FT HELIX 2192 2195
FT TURN 2197 2198
FT STRAND 2206 2206
FT STRAND 2215 2216
FT TURN 2224 2225
FT STRAND 2226 2230
FT STRAND 2236 2240
FT HELIX 2245 2258
FT TURN 2259 2259
SQ SEQUENCE 2291 AA; 265739 MW; 5CDPBOC548BHC39B CRC64;

Query Match 8.6%; Score 19; DB 1; Length 2291;
Best Local Similarity 100.0%; Pred. No. 9,7e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 75 LKLELVSGERLPKPTKG 93
Db 84 LKLELVSGERLPKPTKG 102

RESULT 44
O9TRS2_PIG PRELIMINARY; PRT; 20 AA.
ID O9TRS2_PIG
AC O9TRS2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Spectrin beta SUBUNIT=28 kDa fragment (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sub.
OX NCBI_TaxID=9823;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92209538; PubMed=1555607;
RA Firepiper T., Derancourt J., Pradel L.A.;
RT "Actin and neurofilament binding domain of brain spectrin beta
RT subunit."
RL Eur. J. Biochem. 205:85-91(1992).
DR HSSP; S21195; S21195.
DR HSSP; Q15149; IMB8.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; ACbind actnin.
DR PROSITE; PS00019; ACTININ_1; 1.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2322 MW; F23D09A9EA01F1E CRC64;

Query Match 7.7%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 DERBAVQKKTFTKWNS 53
Db 4 DERBAVQKKTFTKWNS 20
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RESULT 45
O28297_CANFA PRELIMINARY; PRT; 707 AA.
ID O28297_CANFA
AC O28297;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Beta-spectrin (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Trachea;
RX MEDLINE=93176817; PubMed=8439565; DOI=10.1016/0167-4781(93)90299-S;
RA Tan S., Shankar V., Gilmore M.S., Sachdev G.P.;
RT "Nucleotide sequence of a cDNA for canine beta-spectrin reveals high
RT evolutionary conservation."
RL Biochim. Biophys. Acta 1172:217-219(1993).
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; L02897; AAA30879.1; -, mRNA.
DR PIR; S29854; S29854.
DR HSSP; Q62261; 1BTN.
DR SMR; Q28297; 543-648.
DR Ensembl; ENSGAFG00000002744; Canis familiaris.
DR GO; GO:0016040; C:membrane; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00435; Spectrin; 5.
DR PRINTS; PR00683; SPECTRINPH.
DR SMART; SM00233; PH; 1.
DR SMART; SM00150; SPEC; 4.
DR PROSITE; PS50003; PH_DOMAIN; 1.
FT NON_TER 1 1
FT NON_TER 707 707
SQ SEQUENCE 707 AA; 8118 MW; DID6C6CD2108D459 CRC64;

Query Match 7.3%; Score 16; DB 2; Length 707;
Best Local Similarity 100.0%; Pred. No. 3,9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 141 RROQEEERKRRPPSP 156
Db 431 RROQEEERKRRPPSP 446

RESULT 46
O7PSH4_ANOGA PRELIMINARY; PRT; 2296 AA.
ID O7PSH4_ANOGA
AC O7PSH4;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE ENSANGP00000012507.
GN ORFNames=ENSANGC00000010018;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prexygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL "Anopheles gambiae re-annotation."
RN Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
```

RG The Anopheles gambiae Sequence Committee;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAAB0108823; EAA05634.2; -; Genomic_DNA.
 DR HSSP; Q01082; 1BKR.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR001589; Actinin actin bd.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH_type.
 DR InterPro; IPR02017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00435; Spectrin_17.
 DR PRINTS; PR00683; SPECTRINPH.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 KW Actin capping; Actin-binding; Cytoskeleton.
 SQ SEQUENCE 2296 AA; 266023 MW; 1B1974E0F7F4EFO CRC64;
 Query Match 7.3%; Score 16; DB 2; Length 2296;
 Best Local Similarity 100.0%; Pred. No. 1,2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 95 MRHCLENVKXALQPL 110
 Db 104 MRHCLENVKXALQPL 119
 RESULT 47
 Q4RFW3_TETNG PRELIMINARY; PRT; 129 AA.
 AC Q4RFW3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 16 SCAP15113, whole genome shotgun sequence.
 GN ORFNames=GSTENG00035151001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Maucell E., Bouteau V., Fischer C., Ozout-Costaz C., Bernot A.,
 RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Daeslija C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Antouard V., Jubin C., Castelli V., Katinka M., Vachere B.,
 RA Bismont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Patra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Queller F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander B.S., Weissbach J., Roest Crolius H.;
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP Genoscope; Whitehead Institute Centre for Genome Research;
 RG Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAAB0105113; CAG12719.1; -; Genomic_DNA.
 SQ SEQUENCE 129 AA; 14599 MW; CSB34F14E04E7ELC CRC64;
 Query Match 6.8%; Score 15; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 8.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 41 AVOKKFTKWNNSHL 55
 Db 53 AVOKKFTKWNNSHL 67
 RESULT 48
 Q9U9J7_CAEEL PRELIMINARY; PRT; 2257 AA.
 ID Q9U9J7_CAEEL
 AC Q9U9J7
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Beta-g spectrin (Beta-spectrin) (uncoordinated protein 70, isoform
 DE a).
 GN Name=bgs-1; Synonyms=unc-70; ORFNames=KL1C4.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Moorthy S., Chen L., Bennett V.,
 RT "Caenorhabditis elegans beta-g spectrin is dispensable for
 RT establishment of epithelial polarity, but essential for muscular and
 RT neuronal function.";
 RL J. Cell. Biochem. 149:915-930(2000).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=20273916; PubMed=10811832; DOI=10.1083/jcb.149.4.931;
 RA Hammariund M., Davis W.S., Jorgensen E.M.;
 RT "Mutations in beta-spectrin disrupt axon outgrowth and sarcomere
 RT structure.";
 RL J. Cell Biol. 149:931-942(2000).
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 CC -!- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AF16170; AAD49859.1; -; mRNA.
 DR EMBL; AF21891; AAF72996.1; -; mRNA.
 DR EMBL; U64854; AAK77611.1; -; Genomic_DNA.
 DR HSSP; Q01082; 1BKR.
 DR Ensembl; KL1C4.3; Caenorhabditis elegans.
 DR WormBase; WBGene0006803; KL1C4.3.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR001589; Actinin actin bd.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH_type.
 DR InterPro; IPR02017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00435; Spectrin_17.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00150; SPC; 17.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.

DR PROSITE; PS50003; PH DOMAIN; 1.
 KW Actin capping; Actin-binding; Complete proteome; Cytoskeleton.
 SQ SEQUENCE 2257 AA; 262228 MW; E1393B6D0914D803 CRC64;

Query Match 6.4%; Score 14; DB 2; Length 2257;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKVNNSHL 55
 |||||
 DB 41 VOKKFTKVNNSHL 54

RESULT 49

060WP8 CAEBR PRELIMINARY; PRT; 2299 AA.

ID 060WP8 CAEBR PRELIMINARY; PRT; 2299 AA.
 AC 060WP8;
 DT 25-OCT-2004 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Hypothetical protein CBG19038 (Fragment).
 GN Name=CBG19038;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_Taxid=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C. briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; CAC01000098; CAB1967.1; Genomic_DNA.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR001589; Actin_actin_bd.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR002017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00435; Spectrin; 17.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00150; SPEC; 17.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 KW Actin capping; Actin-binding; Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 2299 AA; 267209 MW; 356A428563A4462 CRC64;

Query Match 6.4%; Score 14; DB 2; Length 2299;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKVNNSHL 55
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 DB 38 VOKKFTKVNNSHL 51

RESULT 50

095ZL8 CAEBL PRELIMINARY; PRT; 2302 AA.

ID 095ZL8 CAEBL PRELIMINARY; PRT; 2302 AA.
 AC 095ZL8;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Uncoordinated protein 70, isoform b.
 GN Name=unc-70; ORFNames=K11C4.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_Taxid=6239;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology";
 RL Science 282:2012-2018(1998).

CC -1- SIMILARITY: Contains 1 PH domain.

DR EMBL; U64854; AA07612.2; Genomic_DNA.
 DR HSSP; Q01082; 1BKR.

DR Ensembl; K11C4.3; Caenorhabditis elegans.
 DR WormBase; WBGene00006803; K11C4.3.

DR WormPep; K11C4.3b; CE30159.

DR GO; GO:0003779; F:actin binding; IEA.

DR InterPro; IPR001589; Actin_actin_bd.
 DR InterPro; IPR001715; Calponin_act_bd.

DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH_type.

DR InterPro; IPR002017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.

DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.

DR Pfam; PF00435; Spectrin; 17.
 DR PRINTS; PR00683; SPECTRINPH.

DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.

DR SMART; SM00150; SPEC; 17.
 DR PROSITE; PS00019; ACTININ_1; 1.

DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.

DR PROSITE; PS50003; PH DOMAIN; 1.
 KW Actin capping; Actin-binding; Complete proteome; Cytoskeleton.

SQ SEQUENCE 2302 AA; 267285 MW; 17E29A016B72E26B CRC64;

Query Match 6.4%; Score 14; DB 2; Length 2302;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKVNNSHL 55
 |||||
 DB 41 VOKKFTKVNNSHL 54

Search completed: March 4, 2006, 07:10:11
 Job time : 285 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 4, 2006, 07:11:46 ; Search time 20 Seconds
(without alignments)

220.005 Million cell updates/sec

Title: US-10-695-994A-7

Perfect score: 220

Sequence: 1 MEIQRITSSIGPLSPAYTQ.....QNYKNFNRRTASDHMSWGM 220

Scoring-table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 135346 seqs, 20000420 residues

Word-size: 6

Total number of hits satisfying chosen parameters: 183

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications_AA_New:*
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	5.0	1452	6 US-10-995-561-778	Sequence 778, App
2	11	5.0	3803	6 US-10-995-561-773	Sequence 772, App
3	11	5.0	3960	6 US-10-995-561-771	Sequence 771, App
4	11	5.0	5406	6 US-10-995-561-774	Sequence 774, App
5	11	5.0	5415	6 US-10-995-561-779	Sequence 779, App
6	11	5.0	5464	6 US-10-995-561-775	Sequence 775, App
7	9	4.1	15	7 US-11-106-932-113	Sequence 113, App
8	9	4.1	30	7 US-11-106-932-33	Sequence 33, App
9	8	3.6	919	6 US-10-821-234-951	Sequence 951, App
10	8	3.6	1089	7 US-11-087-099-7653	Sequence 7653, App
11	8	3.6	1609	7 US-11-087-099-4181	Sequence 4181, App
12	7	3.2	186	7 US-11-072-512-3726	Sequence 3726, App
13	7	3.2	306	6 US-10-995-561-702	Sequence 702, App
14	7	3.2	312	6 US-10-995-561-700	Sequence 700, App
15	7	3.2	361	6 US-10-995-561-701	Sequence 701, App
16	7	3.2	364	6 US-10-995-561-699	Sequence 699, App
17	7	3.2	549	7 US-11-072-512-3479	Sequence 3479, App
18	7	3.2	595	7 US-11-087-099-2273	Sequence 2273, App
19	7	3.2	673	7 US-11-072-512-2425	Sequence 2425, App
20	7	3.2	1099	6 US-10-873-528-11	Sequence 11, App
21	7	3.2	4374	7 US-11-128-572-2	Sequence 2, App
22	7	3.2	5335	6 US-10-995-561-777	Sequence 777, App
23	6	2.7	8	7 US-11-045-024-2635	Sequence 2635, App
24	6	2.7	8	7 US-11-045-024-5011	Sequence 5011, App
25	6	2.7	9	7 US-11-045-024-2649	Sequence 2649, App

26	6	2.7	9	7 US-11-045-024-3576	Sequence 3576, App
27	6	2.7	9	7 US-11-045-024-5023	Sequence 5023, App
28	6	2.7	9	7 US-11-045-024-6897	Sequence 6897, App
29	6	2.7	9	7 US-11-045-024-10720	Sequence 10720, App
30	6	2.7	9	7 US-11-045-024-12456	Sequence 12456, App
31	6	2.7	9	7 US-11-045-024-14001	Sequence 14001, App
32	6	2.7	10	7 US-11-045-024-3582	Sequence 3582, App
33	6	2.7	10	7 US-11-045-024-3582	Sequence 5043, App
34	6	2.7	10	7 US-11-045-024-10716	Sequence 10716, App
35	6	2.7	10	7 US-11-045-024-12492	Sequence 12492, App
36	6	2.7	10	7 US-11-045-024-12853	Sequence 12853, App
37	6	2.7	15	7 US-11-045-024-13345	Sequence 13345, App
38	6	2.7	15	7 US-11-045-024-13348	Sequence 13348, App
39	6	2.7	15	7 US-11-045-024-13515	Sequence 13515, App
40	6	2.7	15	7 US-11-045-024-13516	Sequence 13516, App
41	6	2.7	35	7 US-11-096-725-28	Sequence 28, App
42	6	2.7	100	7 US-11-107-096-78	Sequence 78, App
43	6	2.7	109	7 US-11-053-076-59	Sequence 59, App
44	6	2.7	113	6 US-10-485-788A-724	Sequence 724, App
45	6	2.7	113	7 US-11-053-076-94	Sequence 94, App
46	6	2.7	126	7 US-11-055-822-146	Sequence 146, App
47	6	2.7	134	7 US-11-052-554A-88	Sequence 88, App
48	6	2.7	145	7 US-11-087-099-7788	Sequence 7788, App
49	6	2.7	163	6 US-10-510-386-194	Sequence 194, App
50	6	2.7	165	7 US-11-087-099-5484	Sequence 5484, App
51	6	2.7	184	7 US-11-084-591-5	Sequence 5, App
52	6	2.7	184	7 US-11-087-099-5689	Sequence 5689, App
53	6	2.7	185	6 US-10-793-626-2102	Sequence 2102, App
54	6	2.7	191	7 US-11-176-830-875	Sequence 875, App
55	6	2.7	215	7 US-11-089-551A-15	Sequence 15, App
56	6	2.7	226	6 US-10-511-538-194	Sequence 194, App
57	6	2.7	237	7 US-11-083-055-2	Sequence 2, App
58	6	2.7	245	7 US-11-098-686-11081	Sequence 11081, App
59	6	2.7	247	7 US-11-098-686-10406	Sequence 10406, App
60	6	2.7	251	7 US-11-098-686-10800	Sequence 10800, App
61	6	2.7	264	6 US-10-467-657-1332	Sequence 1332, App
62	6	2.7	264	7 US-11-087-099-1412	Sequence 412, App
63	6	2.7	271	7 US-11-089-551A-17	Sequence 17, App
64	6	2.7	281	7 US-11-087-099-6709	Sequence 6709, App
65	6	2.7	281	7 US-11-087-099-7386	Sequence 7386, App
66	6	2.7	284	6 US-10-873-528-40	Sequence 40, App
67	6	2.7	286	7 US-11-087-099-4420	Sequence 4420, App
68	6	2.7	286	7 US-11-087-099-4492	Sequence 4492, App
69	6	2.7	286	7 US-11-087-099-6943	Sequence 6943, App
70	6	2.7	286	7 US-11-087-099-7513	Sequence 7513, App
71	6	2.7	286	7 US-11-087-099-8943	Sequence 8943, App
72	6	2.7	287	7 US-11-087-099-9180	Sequence 9180, App
73	6	2.7	287	7 US-11-087-099-9180	Sequence 9180, App
74	6	2.7	287	7 US-11-087-099-8561	Sequence 8561, App
75	6	2.7	287	7 US-11-087-099-11384	Sequence 11384, App
76	6	2.7	296	7 US-11-074-176-22	Sequence 22, App
77	6	2.7	310	7 US-11-087-099-11105	Sequence 11105, App
78	6	2.7	322	7 US-11-073-605-4	Sequence 4, App
79	6	2.7	322	7 US-11-140-284-6	Sequence 6, App
80	6	2.7	324	7 US-11-087-099-10611	Sequence 10611, App
81	6	2.7	331	7 US-11-087-099-9511	Sequence 9511, App
82	6	2.7	333	7 US-11-087-099-490	Sequence 490, App
83	6	2.7	333	7 US-11-087-099-6265	Sequence 6265, App
84	6	2.7	336	7 US-11-087-099-8846	Sequence 8846, App
85	6	2.7	354	7 US-11-087-099-6791	Sequence 6791, App
86	6	2.7	355	7 US-11-087-099-994	Sequence 994, App
87	6	2.7	366	6 US-11-098-686-10689	Sequence 10689, App
88	6	2.7	364	6 US-10-131-826A-186	Sequence 186, App
89	6	2.7	364	6 US-10-973-1158-186	Sequence 186, App
90	6	2.7	370	7 US-11-073-605-2	Sequence 2, App
91	6	2.7	370	7 US-11-075-4005-14	Sequence 14, App
92	6	2.7	370	7 US-11-140-284-8	Sequence 8, App
93	6	2.7	376	6 US-10-517-939-102	Sequence 102, App
94	6	2.7	379	7 US-11-087-099-872	Sequence 872, App
95	6	2.7	387	7 US-11-087-099-11673	Sequence 11673, App
96	6	2.7	391	7 US-11-087-099-10130	Sequence 10130, App
97	6	2.7	409	7 US-11-087-099-2414	Sequence 2414, App
98	6	2.7	411	7 US-11-092-168-8	Sequence 8, App

99	6	2.7	421	7	US-11-072-512-3536	Sequence 3536, Ap
100	6	2.7	429	7	US-11-053-185-2	Sequence 2, Appl
101	6	2.7	432	6	US-10-467-657-8783	Sequence 8783, Ap
102	6	2.7	445	6	US-10-821-234-1506	Sequence 1506, Ap
103	6	2.7	451	7	US-11-087-099-4574	Sequence 4574, Ap
104	6	2.7	452	7	US-11-186-284-79	Sequence 79, Appl
105	6	2.7	452	7	US-11-087-099-2368	Sequence 2368, Ap
106	6	2.7	452	7	US-11-087-099-8208	Sequence 8208, Ap
107	6	2.7	455	5	US-09-978-360A-523	Sequence 523, App
108	6	2.7	459	7	US-11-087-099-8118	Sequence 8118, Ap
109	6	2.7	465	6	US-10-793-628-2828	Sequence 2828, Ap
110	6	2.7	468	6	US-10-957-589-28	Sequence 28, Appl
111	6	2.7	468	7	US-11-097-589-26	Sequence 26, Appl
112	6	2.7	470	6	US-10-878-556A-101	Sequence 101, App
113	6	2.7	471	7	US-11-098-686-11324	Sequence 11324, A
114	6	2.7	478	7	US-11-098-686-10246	Sequence 10246, A
115	6	2.7	479	6	US-10-821-234-871	Sequence 871, App
116	6	2.7	480	7	US-11-087-099-8522	Sequence 8522, Ap
117	6	2.7	481	6	US-10-508-263-28	Sequence 28, Appl
118	6	2.7	485	7	US-11-072-512-3419	Sequence 3419, Ap
119	6	2.7	487	7	US-11-072-512-2868	Sequence 2868, Ap
120	6	2.7	498	7	US-11-072-512-3191	Sequence 3191, Ap
121	6	2.7	499	7	US-11-087-099-1159	Sequence 1159, Ap
122	6	2.7	499	7	US-11-087-099-5941	Sequence 5941, Ap
123	6	2.7	516	6	US-10-508-263-26	Sequence 26, Appl
124	6	2.7	518	7	US-11-072-512-3059	Sequence 3059, Ap
125	6	2.7	539	6	US-10-467-657-6792	Sequence 6792, Ap
126	6	2.7	562	6	US-10-508-263-24	Sequence 24, Appl
127	6	2.7	567	6	US-10-330-773-556	Sequence 556, App
128	6	2.7	582	6	US-10-330-773-558	Sequence 558, App
129	6	2.7	612	6	US-10-467-657-764	Sequence 764, App
130	6	2.7	620	6	US-10-330-773-75	Sequence 75, Appl
131	6	2.7	629	7	US-11-098-686-11359	Sequence 11359, A
132	6	2.7	643	7	US-11-087-099-1991	Sequence 1991, Ap
133	6	2.7	662	7	US-11-072-175-184	Sequence 184, App
134	6	2.7	664	6	US-10-878-556A-44	Sequence 44, Appl
135	6	2.7	685	7	US-11-089-551A-2	Sequence 2, Appl
136	6	2.7	712	7	US-11-087-099-2922	Sequence 2922, Ap
137	6	2.7	775	6	US-10-858-730-77	Sequence 77, Appl
138	6	2.7	792	7	US-11-087-099-1215	Sequence 1215, Ap
139	6	2.7	805	6	US-10-485-517-198	Sequence 198, App
140	6	2.7	853	6	US-10-420-192-6	Sequence 6, Appl
141	6	2.7	908	6	US-10-821-234-1267	Sequence 1267, Ap
142	6	2.7	909	7	US-11-077-619-8	Sequence 8, Appl
143	6	2.7	914	7	US-11-072-512-2923	Sequence 2923, Ap
144	6	2.7	923	7	US-11-087-099-9592	Sequence 9592, Ap
145	6	2.7	936	7	US-11-072-512-2621	Sequence 2621, Ap
146	6	2.7	1045	7	US-11-072-512-2830	Sequence 2830, Ap
147	6	2.7	1047	7	US-11-072-512-2408	Sequence 2408, Ap
148	6	2.7	1085	7	US-11-087-099-11646	Sequence 11646, A
149	6	2.7	1087	7	US-11-117-169-10	Sequence 10, Appl
150	6	2.7	1106	7	US-11-076-427A-16	Sequence 16, Appl
151	6	2.7	1106	7	US-11-075-047A-119	Sequence 119, App
152	6	2.7	1123	7	US-11-019-711-71	Sequence 71, Appl
153	6	2.7	1147	7	US-11-087-099-11762	Sequence 11762, A
154	6	2.7	1148	7	US-11-110-082-29	Sequence 29, Appl
155	6	2.7	1149	7	US-11-110-082-30	Sequence 30, Appl
156	6	2.7	1327	7	US-11-019-711-70	Sequence 70, Appl
157	6	2.7	1342	7	US-11-115-639-2	Sequence 2, Appl
158	6	2.7	1342	7	US-11-115-639-3	Sequence 3, Appl
159	6	2.7	1342	7	US-11-115-639-4	Sequence 4, Appl
160	6	2.7	1342	7	US-11-115-639-5	Sequence 5, Appl
161	6	2.7	1342	7	US-11-115-639-6	Sequence 6, Appl
162	6	2.7	1347	7	US-11-087-099-5370	Sequence 5370, Ap
163	6	2.7	1360	7	US-11-241-056-14	Sequence 14, Appl
164	6	2.7	1381	6	US-10-467-657-178	Sequence 178, Appl
165	6	2.7	1381	6	US-10-467-657-3726	Sequence 3726, Ap
166	6	2.7	1562	6	US-11-052-554A-211	Sequence 211, App
167	6	2.7	1565	6	US-10-467-657-2704	Sequence 2704, Ap
168	6	2.7	1681	7	US-11-019-711-20	Sequence 20, Appl
169	6	2.7	1697	7	US-11-019-711-68	Sequence 68, Appl
170	6	2.7	1723	7	US-11-019-711-18	Sequence 18, Appl
171	6	2.7	1897	6	US-10-821-234-1635	Sequence 1635, Ap

172	6	2.7	1907	7	US-11-000-463-250	Sequence 250, App
173	6	2.7	1976	7	US-11-069-834-52	Sequence 52, Appl
174	6	2.7	1976	7	US-11-069-834-54	Sequence 54, Appl
175	6	2.7	2117	7	US-11-087-099-9594	Sequence 9594, Ap
176	6	2.7	2515	7	US-11-113-424-53	Sequence 53, Appl
177	6	2.7	2640	7	US-11-087-099-11966	Sequence 11966, A
178	6	2.7	2647	6	US-10-821-234-1303	Sequence 1303, Ap
179	6	2.7	2657	6	US-10-821-234-1262	Sequence 1262, Ap
180	6	2.7	3674	7	US-11-000-463-454	Sequence 454, App
181	6	2.7	4384	6	US-10-821-234-1120	Sequence 1120, Ap
182	6	2.7	5291	7	US-11-052-554A-281	Sequence 281, App
183	6	2.7	8746	7	US-11-098-686-10232	Sequence 10232, A

ALIGNMENTS

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RESULT 1
US-10-995-561-778
; Sequence 778, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778
; LENGTH: 1452
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-995-561-778

Query Match
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKWN 52
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Db 79 VOKKTFTKWN 89

RESULT 2
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-995-561-773

Query Match
Best Local Similarity 5.0%; Score 11; DB 6; Length 3803;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKWN 52
|||||
Db 79 VOKKTFTKWN 89
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RESULT 3
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-771

Query Match
Best Local Similarity 5.0%; Score 11; DB 6; Length 3960;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWN 52
Db 79 VOKKFTKWN 89

RESULT 4
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match
Best Local Similarity 5.0%; Score 11; DB 6; Length 5406;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWN 52
Db 79 VOKKFTKWN 89

RESULT 5
US-10-995-561-779
; Sequence 779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-779

Query Match
Best Local Similarity 5.0%; Score 11; DB 6; Length 5415;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWN 52
Db 79 VOKKFTKWN 89

RESULT 6
US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match
Best Local Similarity 5.0%; Score 11; DB 6; Length 5464;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWN 52
Db 79 VOKKFTKWN 89

RESULT 7
US-11-106-932-113
; Sequence 113, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-113

Query Match
Best Local Similarity 4.1%; Score 9; DB 7; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 LPAEQSPR 192
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Db 1 LPAEQGSPR 9

RESULT 8

US-11-106-932-33
; Sequence 33, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 30
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-106-932-33

Query Match 4.1%; Score 9; DB 7; Length 30;
Best Local Similarity 100.0%; Pred.No.0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 LPAEQGSPR 192

Db 1 LPAEQGSPR 9

RESULT 9

US-10-821-234-951
; Sequence 951, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 951
; LENGTH: 919
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-821-234-951

Query Match 3.6%; Score 8; DB 6; Length 919;
Best Local Similarity 100.0%; Pred.No.4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 SGERLPKP 90

Db 96 SGERLPKP 103

RESULT 10

US-11-087-099-7653
; Sequence 7653, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7653
; LENGTH: 1089
; TYPE: PRF
; ORGANISM: Streptomyces coelicolor A3(2)

US-11-087-099-7653

Query Match 3.6%; Score 8; DB 7; Length 1089;
Best Local Similarity 100.0%; Pred.No.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 EEBERKR 152

Db 761 EEBERKR 768

RESULT 11

US-11-087-099-4181
; Sequence 4181, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4181
; LENGTH: 1609
; TYPE: PRF
; ORGANISM: Neurospora crassa
US-11-087-099-4181

Query Match 3.6%; Score 8; DB 7; Length 1609;
Best Local Similarity 100.0%; Pred.No.7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 EEBERKR 151

Db 1191 EEBERKR 1198

RESULT 12

US-11-072-512-3726
; Sequence 3726, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TENSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978

; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3726
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3726

Query Match 3.2%; Score 7; DB 7; Length 186;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 RPPSPDP 158
Db 103 RPPSPDP 109

RESULT 13

US-10-995-561-702
; Sequence 702, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 702
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-702

Query Match 3.2%; Score 7; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LKEQRVH 116
Db 144 LKEQRVH 150

RESULT 14

US-10-995-561-700
; Sequence 700, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-700

Query Match 3.2%; Score 7; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LKEQRVH 116
Db 199 LKEQRVH 205

RESULT 15

US-10-995-561-701
; Sequence 701, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-701

Query Match 3.2%; Score 7; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LKEQRVH 116
Db 199 LKEQRVH 205

RESULT 16

US-10-995-561-699
; Sequence 699, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-699

Query Match 3.2%; Score 7; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LKEQRVH 116
Db 199 LKEQRVH 205

RESULT 17

US-11-072-512-3479
; Sequence 3479, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHITAKA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 08435-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3479
LENGTH: 549
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3479

Query Match 3.2% Score 7, DB 7, Length 549,
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 112 EQRVHLE 118
DB 28 EQRVHLE 34

RESULT 18
US-11-087-099-2273
Sequence 2273, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2273
LENGTH: 595
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-11-087-099-2273

Query Match 3.2% Score 7, DB 7, Length 595,
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 80 EYLSGER 86
DB 252 EYLSGER 258

RESULT 19
US-11-072-512-2425
Sequence 2425, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI

APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHITAKA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 08435-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2425
LENGTH: 673
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2425

Query Match 3.2% Score 7, DB 7, Length 673,
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 75 LKLELV 81
DB 516 LKLELV 522

RESULT 20
US-10-873-528-11
Sequence 11, Application US/10873528
Publication No. US20050276814A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hanbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21125WO
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT FILING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 981637.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 1099
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-10-873-528-11

Query Match 3.2% Score 7, DB 6, Length 1099,
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 63 TDLXTDL 69
DB 402 TDLXTDL 408

```
RESULT 21
US-11-128-572-2
; Sequence 2, Application US/11128572
; Publication No. US20050266513A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; TITLE OF INVENTION: Method for identifying compounds that have the potential to inhibit
; FILE REFERENCE: Case 12-0231-PCT
; CURRENT APPLICATION NUMBER: US/11/128,572
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-572-2

Query Match
Best Local Similarity 3.2%; Score 7; DB 7; Length 4374;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 LKLELV 81
DB 1557 LKLELV 1563

RESULT 22
US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

Query Match
Best Local Similarity 3.2%; Score 7; DB 6; Length 5335;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 LLEVLGS 84
DB 23 LLEVLGS 29

RESULT 23
US-11-045-024-2635
; Sequence 2635, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingstone, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
```

```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: Virus-1 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2635
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2635

Query Match
Best Local Similarity 2.7%; Score 6; DB 7; Length 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLELIE 139
DB 1 TLELIE 6

RESULT 24
US-11-045-024-5011
; Sequence 5011, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingstone, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: Virus-1 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
```


;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5011
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5011

Query Match 2.7%; Score 6; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLEBLE 139
|||||
DB 1 TLEBLE 6

RESULT 25
US-11-045-024-2649
; Sequence 2649, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2649
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2649

Query Match 2.7%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLEBLE 139
|||||
DB 2 TLEBLE 7

RESULT 26
US-11-045-024-3576

; Sequence 3576, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3576
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3576

Query Match 2.7%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLEBLE 139
|||||
DB 1 TLEBLE 6

RESULT 27
US-11-045-024-5023
; Sequence 5023, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05

Query Match 2.7%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5023
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5023

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLELLE 139
DB 2 TLELLE 7

RESULT 28
US-11-045-024-6897
; Sequence 6897, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6897
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

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US-11-045-024-6897

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLELLE 139
DB 2 TLELLE 7

RESULT 29
US-11-045-024-10720
; Sequence 10720, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10720
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10720

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLELLE 139
DB 1 TLELLE 6

RESULT 30
US-11-045-024-12496
; Sequence 12496, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
```

```
/ APPLICANT: Cheanut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Beteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12496
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12496
```

```
Query Match          2.7%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      134 TLELLE 139
Db      1 TLELLE 6
```

```
RESULT 31
/ Sequence 14001, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheanut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Beteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
```

```
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14001
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14001
```

```
Query Match          2.7%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      134 TLELLE 139
Db      2 TLELLE 7
```

```
RESULT 32
/ Sequence 3582, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheanut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Beteban
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Kubo, Ralph
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3582
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3582
```

```
Query Match          2.7%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      134 TLELLE 139
```

Db 2 TLELLE 7

```
RESULT 33
US-11-045-024-5043
; Sequence 5043, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5043
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5043

Query Match 2.7% Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLELLE 139
Db 3 TLELLE 8

RESULT 34
US-11-045-024-10716
; Sequence 10716, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
```

```
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10716
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10716

Query Match 2.7% Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLELLE 139
Db 2 TLELLE 7

RESULT 35
US-11-045-024-12492
; Sequence 12492, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
```

NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12492
LENGTH: 10
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12492

Query Match 2.7%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLEFILE 139
DB 2 TLEFILE 7

RESULT 36
US-11-045-024-12853
Sequence 12853, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Estebean
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT FILING DATE: 2005-01-28
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12853
LENGTH: 10
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12853

Query Match 2.7%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLEFILE 139
DB 3 TLEFILE 8

RESULT 37
US-11-045-024-13345
Sequence 13345, Application US/11045024

Publication No. US20050271676A1

GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Estebean
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.

APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT FILING DATE: 2005-01-28
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13345
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13345

Query Match 2.7%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TLEFILE 139
DB 5 TLEFILE 10

RESULT 38
US-11-045-024-13348
Sequence 13348, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Estebean
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.

APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT FILING DATE: 2005-01-28
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146

```
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 13348
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13348
```

```
Query Match          2.7%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      134 TLELLE 139
Db      8 TLELLE 13
```

RESULT 39

```
;; Sequence 13515, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
```

```
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Cells, Esteban
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
```

```
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; FILE REFERENCE: 2060.0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
```

```
;; CURRENT FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 13515
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13515
```

```
Query Match          2.7%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      134 TLELLE 139
Db      1 TLELLE 6
```

RESULT 40

```
;; Sequence 13516, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
```

```
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Cells, Esteban
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
```

```
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; FILE REFERENCE: 2060.0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
```

```
;; CURRENT FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 13516
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13516
```

```
Query Match          2.7%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      134 TLELLE 139
Db      1 TLELLE 6
```

RESULT 41

```
;; Sequence 28, Application US/11096725
;; Publication No. US20060013820A1
;; GENERAL INFORMATION:
```

```
;; APPLICANT: BONNET, Dominique
;; APPLICANT: BROWN, Carlton B
;; APPLICANT: GEORGES, Bertrand
;; APPLICANT: SIZER, Philip J
;; TITLE OF INVENTION: Antigen Delivery Vectors and Constructs
US-11-045-024-13515
```

```
FILE REFERENCE: KLB-001
CURRENT APPLICATION NUMBER: US/11/096,725
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: GBO408164.2
PRIOR FILING DATE: 2004-04-13
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 35
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-11-096-725-28

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TITLE 139
DB 4 TITLE 9

RESULT 42
US-11-107-096-78
Sequence 78, Application US/11/107096
Publication No. US2006000348A1
GENERAL INFORMATION:
APPLICANT: SIDHU, SACHDEV S.
APPLICANT: ZHANG, YINGNAN
TITLE OF INVENTION: OMT PDZ MODULATORS
FILE REFERENCE: P2100R1
CURRENT APPLICATION NUMBER: US/11/107,096
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,157
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 78
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-11-107-096-78

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 100;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LLEVR 142
DB 80 LLEVR 85

RESULT 43
US-11-053-076-59
Sequence 59, Application US/11/053076
Publication No. US20050255460A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Johannes
APPLICANT: Somora Diaz-Samiente, Chamorro
APPLICANT: Belmares, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-008CIP
CURRENT APPLICATION NUMBER: US/11/053,076
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: PCT/US03/28508
PRIOR FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 60/409,298
```

```
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-11-053-076-59

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 109;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LLEVR 142
DB 93 LLEVR 98

RESULT 44
US-10-485-788A-724
Sequence 724, Application US/10/485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-00320US
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 724
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-724

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 113;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 KLEVL 82
DB 22 KLEVL 27

RESULT 45
US-11-053-076-94
Sequence 94, Application US/11/053076
Publication No. US20050255460A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Johannes
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APPLICANT: Somoza Diaz-Sarmiento, Chamorro
APPLICANT: Belmares, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-008CIP
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: PCT/US03/28508
PRIOR FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 60/409,298
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 94
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-11-053-076-94

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 113;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 KLEVL 82
Db 22 KLEVL 27

RESULT 46
US-11-055-822-146
Sequence 146, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroeder, Hartwig
APPLICANT: Zeidler, Oskar
APPLICANT: Haberer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BGI-121CPCN
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-06
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PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 146
LENGTH: 126
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-146

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 126;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LLEVR 142
Db 58 LLEVR 63

RESULT 47
US-11-052-554A-88
Sequence 88, Application US/11052554A
Publication No. US2005028866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
FILE REFERENCE: 30853/40359A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
SEQ ID NO 88
LENGTH: 134
TYPE: PRT
ORGANISM: Haemophilus influenzae Rd
US-11-052-554A-88

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 134;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VDKALQ 108
Db 36 VDKALQ 41

RESULT 48
US-11-087-099-7788
Sequence 7788, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7788
LENGTH: 145
TYPE: PRT
ORGANISM: Zea mays
US-11-087-099-7788

Query Match
Best Local Similarity 100.0%; Score 6; DB 7; Length 145;
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Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 QOEER 148
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Db 130 QOEER 135
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RESULT 49

US-10-510-386-194
; Sequence 194, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 194
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-194

Query Match

Best Local Similarity 100.0%; Score 6; DB 6; Length 163;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 TKVNS 53
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Db 27 TKVNS 32
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RESULT 50

US-11-087-099-5484
; Sequence 5484, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B BP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5484
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-11-087-099-5484

Query Match

Best Local Similarity 100.0%; Score 6; DB 7; Length 165;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ISGPLS 14
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Db 104 ISGPLS 109
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Title: US-10-695-994a-7

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and is derived by analysis of the total score distribution.

SUMMARIES

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5	97	44.1	1630	US-10-170-385-15	Sequence 15, Appl
6	38	17.3	57	US-09-945-917-43	Sequence 43, Appl
7	38	17.3	2106	US-10-408-765A-2093	Sequence 2093, Ap
8	38	17.3	2137	US-10-756-149-4806	Sequence 4806, Ap
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17	15	6.8	17	US-10-862-195-1551	Sequence 1551, Ap
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21	11	5.0	1355	US-10-369-493-5252	Sequence 5252, Ap
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97	7	3.2	158	US-10-501-282-4406	Sequence 4406, App
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111	7	3.2	205	4	US-10-425-115-215289	Sequence 215289,	184	7	3.2	549	4	US-10-104-047-3479	Sequence 3479, App
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113	7	3.2	218	4	US-10-029-386-32067	Sequence 32067, A	186	7	3.2	554	5	US-10-830-828-8	Sequence 8, Appl1
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118	7	3.2	233	4	US-10-156-761-14807	Sequence 14807, A	191	7	3.2	597	4	US-10-437-963-181830	Sequence 181830,
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120	7	3.2	246	4	US-10-425-115-233921	Sequence 233921,	193	7	3.2	600	4	US-10-092-900A-124	Sequence 124, App
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125	7	3.2	263	4	US-10-425-115-327227	Sequence 327227,	198	7	3.2	656	3	US-10-437-963-175977	Sequence 175977,
126	7	3.2	271	4	US-10-659-755-14	Sequence 14, Appl	199	7	3.2	656	4	US-10-989-228-30	Sequence 30, Appl
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134	7	3.2	298	4	US-10-425-114-48246	Sequence 48246, A	207	7	3.2	699	5	US-10-785-823-7	Sequence 7, Appl1
135	7	3.2	302	4	US-10-425-114-68383	Sequence 68383, A	208	7	3.2	701	4	US-10-282-122A-66828	Sequence 66828, A
136	7	3.2	304	4	US-10-425-115-344502	Sequence 344502,	209	7	3.2	701	4	US-10-282-122A-69334	Sequence 69324, A
137	7	3.2	306	4	US-10-724-972A-4481	Sequence 4481, Ap	210	7	3.2	702	4	US-10-369-493-4024	Sequence 4024, Ap
138	7	3.2	314	5	US-10-450-763-33610	Sequence 33610, A	211	7	3.2	702	4	US-10-282-122A-67653	Sequence 67653, A
139	7	3.2	316	4	US-10-351-334-3239	Sequence 3239, App	212	7	3.2	705	4	US-10-389-566-2111	Sequence 2111, Ap
140	7	3.2	321	4	US-10-351-334-355	Sequence 355, App	213	7	3.2	717	4	US-10-369-493-4154	Sequence 4154, Ap
141	7	3.2	326	5	US-10-489-372-18	Sequence 18, Appl	214	7	3.2	730	4	US-10-131-827-8768	Sequence 8768, Ap
142	7	3.2	326	5	US-10-994-726-672	Sequence 672, App	215	7	3.2	731	4	US-10-108-260A-2451	Sequence 2451, Ap
143	7	3.2	329	5	US-10-501-282-5654	Sequence 5654, Ap	216	7	3.2	731	4	US-10-108-260A-2451	Sequence 2451, Ap
144	7	3.2	344	4	US-10-425-115-232166	Sequence 232166,	217	7	3.2	731	5	US-10-450-763-47811	Sequence 47811, Ap
145	7	3.2	344	5	US-10-732-923-10148	Sequence 10148, A	218	7	3.2	737	3	US-09-955-732-13	Sequence 13, Appl
146	7	3.2	344	6	US-11-097-143-3432	Sequence 3432, Ap	219	7	3.2	764	3	US-09-740-043-4	Sequence 4, Appl1
147	7	3.2	357	5	US-10-994-726-671	Sequence 671, App	220	7	3.2	764	4	US-10-072-012-543	Sequence 543, App
148	7	3.2	357	5	US-10-732-923-10043	Sequence 10043, A	221	7	3.2	836	4	US-10-437-963-12282	Sequence 12282,
149	7	3.2	357	5	US-10-732-923-10066	Sequence 10066, A	222	7	3.2	854	5	US-10-756-149-5164	Sequence 5164, Ap
150	7	3.2	357	5	US-10-732-923-10066	Sequence 10066, A	223	7	3.2	857	4	US-10-425-114-45539	Sequence 45539, A
151	7	3.2	358	5	US-10-732-923-10067	Sequence 10067, A	224	7	3.2	857	4	US-10-425-115-205907	Sequence 205907,
152	7	3.2	358	6	US-11-069-633-45	Sequence 45, Appl	225	7	3.2	861	6	US-11-097-143-15876	Sequence 15876, A
153	7	3.2	362	4	US-10-489-372-19	Sequence 19, Appl	226	7	3.2	871	6	US-11-097-143-1638	Sequence 1638, Ap
154	7	3.2	366	5	US-10-491-823-203	Sequence 203, App	227	7	3.2	876	5	US-10-830-828-6	Sequence 6, Appl1
155	7	3.2	366	5	US-10-911-823-328	Sequence 328, App	228	7	3.2	876	5	US-10-830-828-6	Sequence 6, Appl1
156	7	3.2	367	5	US-10-732-923-10111	Sequence 10111, A	229	7	3.2	900	4	US-10-408-765A-1502	Sequence 1502, Ap
157	7	3.2	368	5	US-10-732-923-10107	Sequence 10107, A	230	7	3.2	923	5	US-10-732-923-18453	Sequence 18453, A
158	7	3.2	368	5	US-10-732-923-10108	Sequence 10108, A	231	7	3.2	956	4	US-10-108-260A-3037	Sequence 3037, Ap
159	7	3.2	368	5	US-10-732-923-10109	Sequence 10109, A	232	7	3.2	960	4	US-10-437-963-187517	Sequence 187517,
160	7	3.2	373	4	US-10-701-919-4	Sequence 4, Appl1	233	7	3.2	977	4	US-10-425-115-272448	Sequence 272448,
161	7	3.2	379	4	US-10-425-115-202498	Sequence 202498,	234	7	3.2	1045	6	US-11-097-143-13350	Sequence 13350, A
162	7	3.2	389	4	US-10-437-963-199329	Sequence 199329,	235	7	3.2	1074	4	US-10-389-566-2371	Sequence 2371, Ap
163	7	3.2	393	4	US-10-369-493-13923	Sequence 13923, A	236	7	3.2	1088	4	US-10-424-599-191750	Sequence 191750,
164	7	3.2	402	4	US-10-437-963-188201	Sequence 188201,	237	7	3.2	1091	4	US-10-282-122A-73976	Sequence 73976, A
165	7	3.2	410	4	US-10-437-963-182626	Sequence 182626,	238	7	3.2	1099	3	US-09-769-787-11	Sequence 11, Appl
166	7	3.2	418	4	US-10-424-599-240813	Sequence 240813,	239	7	3.2	1100	5	US-10-472-928-2300	Sequence 2300, Ap
167	7	3.2	422	4	US-10-128-714-3539	Sequence 3539, Ap	240	7	3.2	1100	5	US-10-494-944-22	Sequence 22, Appl
168	7	3.2	422	4	US-10-128-714-8539	Sequence 8539, Ap	241	7	3.2	1102	5	US-10-617-320-4859	Sequence 4859, Ap
169	7	3.2	426	5	US-10-501-282-5656	Sequence 5656, Ap	242	7	3.2	1118	5	US-10-732-923-8271	Sequence 8271, Ap
170	7	3.2	431	4	US-10-424-599-148023	Sequence 148023,	243	7	3.2	1135	4	US-09-972-221-108	Sequence 108, App
171	7	3.2	433	4	US-10-309-175-4	Sequence 4, Appl1	244	7	3.2	1135	4	US-10-096-628-108	Sequence 108, App
172	7	3.2	433	4	US-10-437-963-118208	Sequence 118208,	245	7	3.2	1146	4	US-10-316-532-2	Sequence 2, Appl1
173	7	3.2	434	4	US-10-424-599-148200	Sequence 148200,	246	7	3.2	1150	4	US-10-316-533-4	Sequence 4, Appl1

247	7	3.2	1150	4	US-10-433-544-4	Sequence 4, Appl1	320	2.7	39	3	US-09-864-761-41697	Sequence 41697, A
248	7	3.2	1153	5	US-10-828-815-33	Sequence 133, Appl	321	2.7	39	4	US-10-312-691-4	Sequence 4, Appl1
249	7	3.2	1161	4	US-10-032-189-133	Sequence 133, App	322	2.7	39	4	US-10-425-115-33435	Sequence 33435, A
250	7	3.2	1162	4	US-10-094-749-2705	Sequence 2705, Ap	323	2.7	40	4	US-10-038-612-56	Sequence 56, Appl
251	7	3.2	1172	5	US-10-828-815-35	Sequence 35, Appl	324	2.7	40	4	US-10-425-115-185768	Sequence 185768, A
252	7	3.2	1179	3	US-09-972-211-109	Sequence 109, Appl	325	2.7	41	4	US-10-029-386-27473	Sequence 27473, A
253	7	3.2	1202	4	US-10-096-625-109	Sequence 109, App	326	2.7	42	3	US-09-864-761-48522	Sequence 48522, A
254	7	3.2	1265	4	US-10-408-765A-997	Sequence 997, App	327	2.7	42	3	US-09-917-340-69	Sequence 69, Appl
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256	7	3.2	1285	4	US-10-205-823-273	Sequence 273, App	329	2.7	42	5	US-10-909-119-83	Sequence 83, Appl
257	7	3.2	1285	4	US-10-177-293-317	Sequence 317, App	330	2.7	42	5	US-10-657-851-69	Sequence 69, Appl
258	7	3.2	1285	4	US-10-263-929-126	Sequence 126, App	331	2.7	44	5	US-10-794-514A-486	Sequence 486, App
259	7	3.2	1285	6	US-11-051-454-273	Sequence 273, App	332	2.7	45	4	US-10-008-524A-103	Sequence 103, App
260	7	3.2	1311	5	US-10-501-282-3598	Sequence 3598, Ap	333	2.7	45	4	US-10-350-719-103	Sequence 103, App
261	7	3.2	1314	5	US-10-756-149-5672	Sequence 5672, Ap	334	2.7	45	4	US-10-425-115-18666	Sequence 18666, A
262	7	3.2	1336	4	US-10-369-493-1723	Sequence 1723, Ap	335	2.7	45	4	US-10-425-115-35529	Sequence 35529, A
263	7	3.2	1383	5	US-10-501-282-3500	Sequence 3600, Ap	336	2.7	46	4	US-10-724-912A-6620	Sequence 6620, Ap
264	7	3.2	1407	5	US-10-732-923-3359	Sequence 3359, Ap	337	2.7	47	4	US-10-437-963-147175	Sequence 147175, A
265	7	3.2	1583	4	US-10-437-963-159486	Sequence 159486, A	338	2.7	48	4	US-10-425-115-334970	Sequence 334970, A
266	7	3.2	1644	4	US-10-408-765A-919	Sequence 919, App	339	2.7	49	4	US-10-424-599-553504	Sequence 253504, A
267	7	3.2	2285	5	US-10-773-446-101	Sequence 101, App	340	2.7	50	4	US-10-425-115-218210	Sequence 218210, A
268	7	3.2	2429	5	US-10-732-923-18427	Sequence 18427, A	341	2.7	51	3	US-09-864-761-35058	Sequence 35058, A
269	7	3.2	2440	5	US-10-732-923-18452	Sequence 18452, A	342	2.7	52	3	US-09-971-980-57	Sequence 67, Appl
270	7	3.2	2441	4	US-10-109-886-8	Sequence 8, Appl1	343	2.7	52	4	US-10-437-963-134817	Sequence 134817, A
271	7	3.2	2441	4	US-10-628-957-2	Sequence 2, Appl1	344	2.7	52	4	US-10-437-963-193623	Sequence 193623, A
272	7	3.2	2441	5	US-10-473-127-643	Sequence 643, App	345	2.7	52	5	US-10-966-576-67	Sequence 67, Appl
273	7	3.2	2441	5	US-10-732-923-18428	Sequence 18428, A	346	2.7	53	4	US-10-028-386-29940	Sequence 29940, A
274	7	3.2	2441	5	US-10-732-923-18429	Sequence 18429, A	347	2.7	53	4	US-10-425-115-296394	Sequence 296394, A
275	7	3.2	2442	4	US-10-109-886-10	Sequence 10, Appl	348	2.7	54	4	US-10-424-599-270787	Sequence 270787, A
276	7	3.2	2442	4	US-10-473-127-631	Sequence 631, App	349	2.7	54	4	US-10-425-115-286486	Sequence 286486, A
277	7	3.2	2442	5	US-10-473-127-633	Sequence 633, App	350	2.7	54	4	US-10-425-115-362961	Sequence 362961, A
278	7	3.2	2442	5	US-10-473-127-645	Sequence 645, App	351	2.7	55	4	US-10-424-599-204690	Sequence 204690, A
279	7	3.2	2442	5	US-10-473-127-647	Sequence 647, App	352	2.7	55	4	US-10-425-115-271198	Sequence 271198, A
280	7	3.2	2442	5	US-10-732-923-18450	Sequence 18450, A	353	2.7	56	3	US-09-864-761-34621	Sequence 34621, A
281	7	3.2	2442	5	US-10-732-923-18451	Sequence 18451, A	354	2.7	58	3	US-09-971-980-69	Sequence 69, Appl
282	7	3.2	2442	5	US-10-840-060-92	Sequence 92, Appl	355	2.7	58	3	US-09-945-917-38	Sequence 38, Appl
283	7	3.2	2442	5	US-10-200-708-103	Sequence 103, App	356	2.7	58	4	US-10-424-599-143876	Sequence 143876, A
284	7	2.7	10	4	US-10-200-708-128	Sequence 128, App	357	2.7	58	5	US-10-966-576-69	Sequence 69, Appl
285	6	2.7	10	4	US-10-200-708-209	Sequence 209, App	358	2.7	59	3	US-09-738-626-6552	Sequence 6552, Ap
286	6	2.7	10	4	US-10-200-708-400	Sequence 400, App	359	2.7	59	3	US-10-437-963-129564	Sequence 129564, A
287	6	2.7	15	3	US-09-876-904A-291	Sequence 291, App	360	2.7	59	5	US-10-450-763-34284	Sequence 34284, A
288	6	2.7	15	4	US-10-461-093-23	Sequence 23, Appl	361	2.7	60	4	US-10-424-599-229175	Sequence 229175, A
289	6	2.7	18	5	US-09-315-355-6	Sequence 6, Appl1	362	2.7	60	4	US-10-425-115-190040	Sequence 190040, A
290	6	2.7	18	5	US-10-848-572-6	Sequence 6, Appl1	363	2.7	60	5	US-10-450-763-11272	Sequence 11272, A
291	6	2.7	19	3	US-09-864-761-40260	Sequence 40260, A	364	2.7	62	4	US-10-767-701-52893	Sequence 52893, A
292	6	2.7	19	5	US-10-813-977-5	Sequence 5, Appl1	365	2.7	62	4	US-10-425-115-334122	Sequence 334122, A
293	6	2.7	20	3	US-09-864-761-44034	Sequence 44034, A	366	2.7	62	4	US-10-425-115-333817	Sequence 333817, A
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295	6	2.7	20	5	US-10-478-112A-3	Sequence 3, Appl1	368	2.7	65	4	US-10-437-963-133003	Sequence 133003, A
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297	6	2.7	20	5	US-10-478-112A-8	Sequence 8, Appl1	370	2.7	65	5	US-10-450-763-37255	Sequence 37255, A
298	6	2.7	20	5	US-10-478-112A-9	Sequence 9, Appl1	371	2.7	66	3	US-09-989-920-219	Sequence 219, App
299	6	2.7	20	5	US-10-478-112A-10	Sequence 10, Appl	372	2.7	67	3	US-09-864-761-33506	Sequence 33506, A
300	6	2.7	20	5	US-10-862-195-677	Sequence 677, App	373	2.7	67	3	US-09-864-761-40606	Sequence 40606, A
301	6	2.7	20	5	US-10-862-195-678	Sequence 678, App	374	2.7	67	4	US-10-425-115-260163	Sequence 260163, A
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304	6	2.7	21	4	US-10-253-493-48	Sequence 48, Appl	377	2.7	68	3	US-09-971-980-63	Sequence 63, Appl
305	6	2.7	21	4	US-09-983-802-305	Sequence 305, App	378	2.7	68	4	US-10-424-599-166978	Sequence 166978, A
306	6	2.7	23	3	US-09-984-450-305	Sequence 450, App	379	2.7	68	4	US-10-424-599-206476	Sequence 206476, A
307	6	2.7	23	3	US-09-973-278-483	Sequence 483, App	380	2.7	68	4	US-10-424-599-274097	Sequence 274097, A
308	6	2.7	25	3	US-09-971-980-71	Sequence 71, Appl	381	2.7	68	4	US-10-425-115-191482	Sequence 191482, A
309	6	2.7	25	4	US-10-053-485-45	Sequence 45, Appl	382	2.7	68	5	US-10-966-576-63	Sequence 63, Appl
310	6	2.7	25	4	US-10-966-576-71	Sequence 71, Appl	383	2.7	69	4	US-10-767-701-454517	Sequence 454517, A
311	6	2.7	31	3	US-11-066-697-1238	Sequence 1238, Ap	384	2.7	69	4	US-10-767-701-60703	Sequence 60703, A
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313	6	2.7	31	5	US-10-966-576-61	Sequence 61, Appl	386	2.7	70	4	US-10-106-698-5831	Sequence 5831, Ap
314	6	2.7	33	4	US-10-425-115-234358	Sequence 234358, A	387	2.7	70	4	US-10-029-386-27874	Sequence 27874, A
315	6	2.7	34	5	US-10-450-763-32778	Sequence 32778, A	388	2.7	70	4	US-10-424-599-229358	Sequence 229358, A
316	6	2.7	35	4	US-10-339-740-254	Sequence 254, App	389	2.7	70	4	US-10-425-115-307725	Sequence 307725, A
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318	6	2.7	36	4	US-10-351-641-760	Sequence 760, App	391	2.7	71	4	US-10-424-599-183419	Sequence 183419, A
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334	6	2.7	72	4	US-10-425-115-354682	Sequence 354682,	467	6	2.7	89	4	US-10-425-115-339997	Sequence 339997,
335	6	2.7	73	4	US-10-425-115-185766	Sequence 185766,	468	6	2.7	89	4	US-10-425-115-351281	Sequence 351281,
336	6	2.7	73	4	US-10-425-115-267758	Sequence 267758,	469	6	2.7	89	6	US-11-097-143-32544	Sequence 32544, A
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402	6	2.7	75	4	US-10-425-115-191322	Sequence 191322,	475	6	2.7	92	3	US-09-864-408A-3954	Sequence 3954, Appl
403	6	2.7	75	4	US-10-425-115-300651	Sequence 300651,	476	6	2.7	92	4	US-10-424-599-335487	Sequence 335487,
404	6	2.7	76	4	US-10-424-599-241422	Sequence 241422,	477	6	2.7	92	4	US-10-424-599-323477	Sequence 323477,
405	6	2.7	76	4	US-10-424-599-258567	Sequence 258567,	478	6	2.7	92	5	US-10-450-763-42232	Sequence 42232, A
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409	6	2.7	76	4	US-10-425-115-340012	Sequence 340012,	482	6	2.7	93	4	US-10-437-963-155946	Sequence 155946,
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412	6	2.7	77	4	US-10-283-618-15	Sequence 15,	485	6	2.7	93	5	US-10-450-763-43747	Sequence 43747, A
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414	6	2.7	78	4	US-10-425-114-58878	Sequence 58878, A	487	6	2.7	94	4	US-10-424-599-243626	Sequence 243626,
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416	6	2.7	78	4	US-10-425-115-325038	Sequence 325038,	489	6	2.7	94	4	US-10-437-963-118987	Sequence 118987,
417	6	2.7	78	5	US-10-113-709A-8	Sequence 8, Appl	490	6	2.7	95	4	US-10-437-963-129100	Sequence 129100,
418	6	2.7	78	5	US-10-994-915-8	Sequence 8, Appl	491	6	2.7	95	4	US-10-425-115-194205	Sequence 194205,
419	6	2.7	79	4	US-10-424-599-159208	Sequence 159208,	492	6	2.7	95	6	US-11-135-597-211	Sequence 211, Appl
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422	6	2.7	79	4	US-10-425-115-266243	Sequence 266243,	495	6	2.7	96	3	US-09-839-329-1	Sequence 1, Appl
423	6	2.7	80	3	US-09-924-358-38	Sequence 38, Appl	496	6	2.7	96	3	US-10-053-261-212	Sequence 212, Appl
424	6	2.7	80	4	US-10-410-764-38	Sequence 38, Appl	497	6	2.7	96	4	US-10-190-435-257	Sequence 257, Appl
425	6	2.7	80	4	US-10-437-963-108889	Sequence 108889,	498	6	2.7	96	4	US-10-190-435-265	Sequence 265, Appl
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431	6	2.7	81	3	US-09-864-408A-1470	Sequence 1470, Appl	504	6	2.7	96	4	US-10-190-435-266	Sequence 266, Appl
432	6	2.7	81	4	US-10-092-154-569	Sequence 569, Appl	505	6	2.7	96	4	US-10-190-435-267	Sequence 267, Appl
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435	6	2.7	82	4	US-10-424-599-256315	Sequence 256315,	508	6	2.7	96	4	US-10-190-435-267	Sequence 267, Appl
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444	6	2.7	84	2	US-08-860-844-77	Sequence 77, Appl	517	6	2.7	96	5	US-10-780-507-65	Sequence 65, Appl
445	6	2.7	84	4	US-10-407-543-77	Sequence 77, Appl	518	6	2.7	96	5	US-10-780-507-66	Sequence 66, Appl
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543	6	2.7	103	4	US-10-425-114-56527	Sequence 50527, A	616	2.7	113	5	US-10-864-252-498	Sequence 498, App
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545	6	2.7	103	4	US-10-437-963-141033	Sequence 141033, A	618	2.7	113	6	US-11-008-889-65	Sequence 65, App1
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609	6	2.7	113	4	US-10-192-381-65	Sequence 94, App1	682	2.7	127	4	US-10-425-114-58027	Sequence 58027, A
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995 6 2.7 216 4 US-10-767-701-44085 Sequence 44085, A
996 6 2.7 216 5 US-10-291-128-144 Sequence 144, App
997 6 2.7 216 5 US-10-953-399-42 Sequence 42, Appl
998 6 2.7 216 6 US-11-097-143-36258 Sequence 36258, A
999 6 2.7 217 4 US-10-424-599-194225 Sequence 194225, A
1000 6 2.7 217 4 US-10-276-774-1679 Sequence 1679, Ap
```

ALIGNMENTS

```
RESULT 1
US-10-695-994-7
; Sequence 7, Application US/10695994
; Publication No. US20040142354A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P04470US1/BAS
; CURRENT FILING DATE: 2003-10-30
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 09/431,184
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-695-994-7
```

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Query Match 100.0%; Score 220; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 7.5e-201;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MEIORTSISGPISPATYGVPPYNNQLEGRFKQLODEREAVOKKFTKWNSHLARVSC 60
DB 1 MEIORTSISGPISPATYGVPPYNNQLEGRFKQLODEREAVOKKFTKWNSHLARVSC 60
QY 61 RITDLYTDLRDGMILKILLEVLSGERLPPYTKGRMRHICLENVDKALQFLKEORVHLEMM 120
DB 61 RITDLYTDLRDGMILKILLEVLSGERLPPYTKGRMRHICLENVDKALQFLKEORVHLEMM 120
QY 121 GSHDIYDGNHRLTTTLELLEVRROQEEBERKRRPPSPDPNTKYSEEAESQOMDTSKGDVYS 180
DB 121 GSHDIYDGNHRLTTTLELLEVRROQEEBERKRRPPSPDPNTKYSEEAESQOMDTSKGDVYS 180
QY 181 QNGLPABOQSPRYVSRYSOYKYNKFNRSRTTASDHSMG 220
DB 181 QNGLPABOQSPRYVSRYSOYKYNKFNRSRTTASDHSMG 220
```

```
RESULT 2
US-10-695-994-4
; Sequence 4, Application US/10695994
; Publication No. US20040142354A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P04470US1/BAS
; CURRENT FILING DATE: 2003-10-30
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 09/431,184
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-695-994-4
```

```
Query Match 56.4%; Score 124; DB 4; Length 2154;
Best Local Similarity 100.0%; Pred. No. 1.2e-108;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 10 GSPISPATYGVPPYNNQLEGRFKQLODEREAVOKKFTKWNSHLARVSCRTDLYTDL 69
DB 10 GSPISPATYGVPPYNNQLEGRFKQLODEREAVOKKFTKWNSHLARVSCRTDLYTDL 69
QY 70 RDGRMLKILLEVLSGERLPPYTKGRMRHICLENVDKALQFLKEORVHLEMMGSHDIVDGN 129
DB 70 RDGRMLKILLEVLSGERLPPYTKGRMRHICLENVDKALQFLKEORVHLEMMGSHDIVDGN 129
QY 130 HRLT 133
DB 130 HRLT 133
```

```
RESULT 3
US-10-805-684-150
; Sequence 150, Application US/10805684
; Publication No. US20050100966A1
; GENERAL INFORMATION:
; APPLICANT: SAKAMOTO, TAKESHI
; APPLICANT: TAKEDA, SHIZU
; TITLE OF INVENTION: PHOS-INTERACTING PROTEINS AND USE THEREOF
; FILE REFERENCE: 58748 (70342)
; CURRENT FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/455,766
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/459,936
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,103
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 150
; LENGTH: 2154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-805-684-150
```

```
Query Match 56.4%; Score 124; DB 5; Length 2154;
Best Local Similarity 100.0%; Pred. No. 1.2e-108;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GSPISPATYGVPPYNNQLEGRFKQLODEREAVOKKFTKWNSHLARVSCRTDLYTDL 69
```

Db 10 SGPSPAYTGQVYNNYNLEGFKQLODEREAVOKKFTKWNVSHLARVSCRITDLYTDL 69
Qy 70 RDGRMLIKLEVLSEGRLPKPTKGMRIHCLENVKALQFLKEQVHLENGSHDIVDGN 129
Db 70 RDGRMLIKLEVLSEGRLPKPTKGMRIHCLENVKALQFLKEQVHLENGSHDIVDGN 129
Qy 130 HRLT 133
130 HRLT 133
130 HRLT 133

RESULT 4
US-10-408-765A-2431

; Sequence 2431, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warrick, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2431
; LENGTH: 1630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2431

Query Match 44.1%; Score 97; DB 4; Length 1630;
Best Local Similarity 100.0%; Pred. No. 4.7e-83;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 DEREAVOKKFTKWNVSHLARVSCRITDLYTDLRDGRMLIKLEVLSEGRLPKPTKGM 96
Db 50 DEREAVOKKFTKWNVSHLARVSCRITDLYTDLRDGRMLIKLEVLSEGRLPKPTKGM 109
Qy 97 IHCLENVKALQFLKEQVHLENGSHDIVDGNHRLT 133
Db 110 IHCLENVKALQFLKEQVHLENGSHDIVDGNHRLT 146

RESULT 5
US-10-170-385-15

; Sequence 15, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; TYPE: PRT

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2364
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-15

Query Match 44.1%; Score 97; DB 4; Length 2364;
Best Local Similarity 100.0%; Pred. No. 6.5e-83;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 DEREAVOKKFTKWNVSHLARVSCRITDLYTDLRDGRMLIKLEVLSEGRLPKPTKGM 96
Db 50 DEREAVOKKFTKWNVSHLARVSCRITDLYTDLRDGRMLIKLEVLSEGRLPKPTKGM 109
Qy 97 IHCLENVKALQFLKEQVHLENGSHDIVDGNHRLT 133
Db 110 IHCLENVKALQFLKEQVHLENGSHDIVDGNHRLT 146

RESULT 6
US-09-945-917-43

; Sequence 43, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joël
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-43

Query Match 17.3%; Score 38; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 MRHCLENVKALQFLKEQVHLENGSHDIVDGNHRL 132
Db 18 MRHCLENVKALQFLKEQVHLENGSHDIVDGNHRL 55

RESULT 7
US-10-408-765A-2093

; Sequence 2093, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warrick, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2093
; LENGTH: 2106
; TYPE: PRT

ORGANISM: Homo sapiens
US-10-408-765A-2093

Query Match 17.3%; Score 38; DB 4; Length 2106;
Best Local Similarity 100.0%; Pred. No. 8.3e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 MRHCLENVDKALQFLKEQRVHLENNGSHDIVDGNRL 132
Db 108 MRHCLENVDKALQFLKEQRVHLENNGSHDIVDGNRL 145

RESULT 8
US-10-756-149-4806
Sequence 4806, Application US/10756149
Publication No. US20050181375A1

GENERAL INFORMATION:
APPLICANT: Aziz, Nacasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file

CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4806
LENGTH: 2137
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-756-149-4806

Query Match 17.3%; Score 38; DB 5; Length 2137;
Best Local Similarity 100.0%; Pred. No. 8.4e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 MRHCLENVDKALQFLKEQRVHLENNGSHDIVDGNRL 132
Db 108 MRHCLENVDKALQFLKEQRVHLENNGSHDIVDGNRL 145

RESULT 9
US-10-972-637-2
Sequence 2, Application US/10972637
Publication No. US20050106659A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: ROTHSTEIN, Jeffrey D.

APPLICANT: JACKSON, Mandy
APPLICANT: LIN, Glen
APPLICANT: LAM, Robert
APPLICANT: ORLOV, Irina
TITLE OF INVENTION: GLUTAMATE TRANSPORTER ASSOCIATED PROTEINS AND METHODS OF USE THEREIN
FILE REFERENCE: JHU1650-2

CURRENT APPLICATION NUMBER: US/10/972,637
CURRENT FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US/09/695,795
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: US 60/161,007
PRIOR FILING DATE: 1999-10-23
PRIOR APPLICATION NUMBER: US 60/206,157
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2

LENGTH: 2388
TYPE: PRT
ORGANISM: Rattus
US-10-972-637-2

Query Match 12.3%; Score 27; DB 5; Length 2388;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LPKPTGMRHICLENVDKALQFLKEQ 113
Db 103 LPKPTGMRHICLENVDKALQFLKEQ 129

RESULT 10
US-10-756-149-5749
Sequence 5749, Application US/10756149
Publication No. US20050181375A1

GENERAL INFORMATION:
APPLICANT: Aziz, Nacasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5749
LENGTH: 2390
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-756-149-5749

Query Match 12.3%; Score 27; DB 5; Length 2390;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LPKPTGMRHICLENVDKALQFLKEQ 113
Db 103 LPKPTGMRHICLENVDKALQFLKEQ 129

RESULT 11
US-09-945-917-40
Sequence 40, Application US/09945917
Publication No. US20030042381A1

GENERAL INFORMATION:
APPLICANT: Bogaert, Thierry
APPLICANT: Vandekechove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P/14-1

CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 51
TYPE: PRT

ORGANISM: Caenorhabditis elegans
US-09-945-917-40

Query Match 11.4%; Score 25; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 8e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 VOKTFTKWNHSLARVSGRTIDLY 66
Db 16 VOKTFTKWNHSLARVSGRTIDLY 40

RESULT 12
US-10-264-049-2841
Sequence 2841, Application US/10264049
Publication No. US20040005579A1

GENERAL INFORMATION:
APPLICANT: Blise et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2841
LENGTH: 806
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (19)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2841

Query Match 10.5%; Score 23; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 131 RLTLELVRRQGEERKRP 153
Db 699 RLTLELVRRQGEERKRP 721

RESULT 13
US-10-756-149-4730
Sequence 4730, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlocznik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4730
LENGTH: 2559
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-756-149-4730

Query Match 10.0%; Score 22; DB 5; Length 2559;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 DEREAQKKTFTKWNHSLARV 58
Db 57 DEREAQKKTFTKWNHSLARV 78

RESULT 14
US-11-097-143-12420
Sequence 12420, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12420
LENGTH: 2291
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-12420

Query Match 8.6%; Score 19; DB 6; Length 2291;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 75 LKLELVISGERLPKPTKG 93
Db 84 LKLELVISGERLPKPTKG 102

RESULT 15
US-09-945-917-46
Sequence 46, Application US/09945917
Publication No. US20030042381A1
GENERAL INFORMATION:
APPLICANT: Bogaert, Thierry
APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
FILE REFERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 48
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-945-917-46

Query Match 7.3%; Score 16; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 107 LQFLKEQVHLNMG 122
Db 33 LQFLKEQVHLNMG 48

RESULT 16
US-10-862-195-1550
Sequence 1550, Application US/10862195
Publication No. US20050164324A1

GENERAL INFORMATION:
APPLICANT: GIGI, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 1550
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
US-10-862-195-1550

Query Match 6.8%; Score 15; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 QVSQNGLPABQSGPR 192
DB 3 QVSQNGLPABQSGPR 17

RESULT 17
US-10-862-195-1551
Sequence 1551, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:
APPLICANT: GIGI, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 1551
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
US-10-862-195-1551

Query Match 6.8%; Score 15; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 QVSQNGLPABQSGPR 192
DB 3 QVSQNGLPABQSGPR 17

RESULT 18
US-10-695-994-20
Sequence 20, Application US/10695994
Publication No. US20040142354A1
GENERAL INFORMATION:
APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
FILE REFERENCE: P04470US1/BAS
CURRENT APPLICATION NUMBER: US/10/695,994
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: 09/431,184
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US98/08656

PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: US 08/841,349
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 20
LENGTH: 14
TYPE: PRT
ORGANISM: Mus musculus
US-10-695-994-20

Query Match 6.4%; Score 14; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 FNSRRASDHSMSG 219
DB 1 FNSRRASDHSMSG 14

RESULT 19
US-10-369-493-6374
Sequence 6374, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO: 6374
LENGTH: 2326
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-6374

Query Match 6.4%; Score 14; DB 4; Length 2326;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKVNSHL 55
DB 110 VOKKTFTKVNSHL 123

RESULT 20
US-10-369-493-5251
Sequence 5251, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO: 5251
LENGTH: 1355

TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5251

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 1355;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTKWN 52
|||||
DB 79 VOKKFTKWN 89

RESULT 21
US-10-369-493-5252
; Sequence 5252, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5252
; LENGTH: 1355
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5252

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 1355;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTKWN 52
|||||
DB 79 VOKKFTKWN 89

RESULT 22
US-10-408-765A-741
; Sequence 741, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Steven W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 741
; LENGTH: 5373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-741

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 5373;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42 VOKKFTKWN 52
|||||
DB 44 VOKKFTKWN 54

RESULT 23
US-10-805-684-151
; Sequence 151, Application US/10805684
; Publication No. US20050100966A1
; GENERAL INFORMATION:
; APPLICANT: SAKAMOTO, TAKESHI
; APPLICANT: TAKEDA, SHIZU
; TITLE OF INVENTION: PHOS-INTERACTING PROTEINS AND USE THEREOF
; FILE REFERENCE: 58748(70342)
; CURRENT APPLICATION NUMBER: US/10/805,684
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/455,766
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/459,936
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,103
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 151
; LENGTH: 5430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-805-684-151

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 5430;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VOKKFTKWN 52
|||||
DB 79 VOKKFTKWN 89

RESULT 24
US-11-097-143-40200
; Sequence 40200, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEAR ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40200

LENGTH: 7201
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-40200

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 7201;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 LLEVLSERLP 88
DB 29 LLEVLSERLP 39

RESULT 25
US-11-097-143-26253
Sequence 26253, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26253
LENGTH: 5385
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-26253

Query Match
Best Local Similarity 100.0%; Score 10; DB 6; Length 5385;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 OKKFTKVN 52
DB 39 OKKFTKVN 48

RESULT 26
US-11-097-143-28275
Sequence 28275, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28275
LENGTH: 5496
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-28275

Query Match
Best Local Similarity 100.0%; Score 10; DB 6; Length 5496;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 OKKFTKVN 52
DB 150 OKKFTKVN 159

RESULT 27
US-10-363-616-413
Sequence 413, Application US/10363616
Publication No. US2004004181A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 413
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-363-616-413

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKVN 50
DB 37 VOKKFTKVN 45

RESULT 28
US-10-450-763-42286
Sequence 42286, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO: 42286
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (63)..(86)
OTHER INFORMATION: Actinin-type actin-binding domain proteins domain identified
OTHER INFORMATION: by eMATRIX, accession number BL00019B, p-value=1.000e-16, raw scc
OTHER INFORMATION: of 13.34
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (35)..(115)
OTHER INFORMATION: Calponin homology (CH) domain identified by Pfam, accession
US-10-450-763-42286

Query Match 4.1%; Score 9; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VQKTFPTKW 50
|||||
DB 36 VQKTFPTKW 44

RESULT 29
US-10-425-115-352183
Sequence 352183, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 352183
LENGTH: 123
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_84355C.1.pep
US-10-425-115-352183

Query Match 4.1%; Score 9; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 QOEERERR 151
|||||
DB 75 QOEERERR 83

RESULT 30
US-10-424-599-237993
Sequence 237993, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 237993
LENGTH: 202
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_56934C.1.pep
US-10-424-599-237993

Query Match 4.1%; Score 9; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 QOEERERR 151
|||||
DB 156 QOEERERR 164

RESULT 31
US-10-425-114-60052
Sequence 60052, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 60052
LENGTH: 202
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3637-254-C10_Flt.pep
US-10-425-114-60052

Query Match 4.1%; Score 9; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 QOEERERR 151
|||||
DB 154 QOEERERR 162

RESULT 32
US-10-425-114-65298
Sequence 65298, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28

```
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 65298
/ LENGTH: 205
/ TYPE: PRT
/ ORGANISM: Zea mays subsp. mexicana
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZMR0TOSINT021B06_FLI.pep
US-10-425-114-65298

Query Match          4.1% Score 9; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      143 OOEERKR 151
DB      157 OOEERKR 165

RESULT 33
US-10-425-114-36959
/ Sequence 36959, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 36959
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB170-019-F4_FLI.pep
US-10-425-114-36959

Query Match          4.1% Score 9; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      143 OOEERKR 151
DB      194 OOEERKR 202

RESULT 34
US-10-408-765A-731
/ Sequence 731, Application US/10408765A
/ Publication No. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Bojn D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
/ FILE REFERENCE: 660088.465
/ CURRENT APPLICATION NUMBER: US/10/408,765A
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 731
/ LENGTH: 3433
```

```
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-408-765A-731

Query Match          4.1% Score 9; DB 4; Length 3433;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 VOKKTFTKW 50
DB      32 VOKKTFTKW 40

RESULT 35
US-10-408-765A-732
/ Sequence 732, Application US/10408765A
/ Publication No. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Bojn D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
/ FILE REFERENCE: 660088.465
/ CURRENT APPLICATION NUMBER: US/10/408,765A
/ CURRENT FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 732
/ LENGTH: 3433
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-408-765A-732

Query Match          4.1% Score 9; DB 4; Length 3433;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 VOKKTFTKW 50
DB      32 VOKKTFTKW 40

RESULT 36
US-10-756-149-5681
/ Sequence 5681, Application US/10756149
/ Publication No. US20050181375A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natsaba
/ APPLICANT: Zlotnick, Albert
/ TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
/ TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
/ FILE REFERENCE: file
/ CURRENT APPLICATION NUMBER: US/10/756,149
/ CURRENT FILING DATE: 2004-01-12
/ NUMBER OF SEQ ID NOS: 5818
/ SOFTWARE: Patencin version 3.2
/ SEQ ID NO 5681
/ LENGTH: 3433
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-756-149-5681

Query Match          4.1% Score 9; DB 5; Length 3433;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 VOKKTFTKW 50
```

Db 32 VOKTFTKW 40

RESULT 37

US-10-767-701-50379
; Sequence 50379, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 50379

LENGTH: 65

TYPE: PRT

ORGANISM: Sorghum bicolor

FEATURE:

OTHER INFORMATION: Clone ID: LIB3480-003-Pl-K1-Pl.pap

US-10-767-701-50379

Query Match

Best Local Similarity 3.6%; Score 8; DB 4; Length 65;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 144 QEEERKR 151

US-10-425-115-368921

RESULT 38

US-10-425-115-368921
; Sequence 368921, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 368921

LENGTH: 177

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(177)

OTHER INFORMATION: unsure at all Xaa locations

OTHER INFORMATION: Clone ID: MRT4577_99631C.1.pap

US-10-425-115-368921

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 196724

LENGTH: 209

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(209)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_110996C.1.pap

US-10-425-115-196724

Query Match

Best Local Similarity 3.6%; Score 8; DB 4; Length 209;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 160 TKVSEAE 167

US-10-437-963-196932

RESULT 40

US-10-437-963-196932
; Sequence 196932, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 196932

LENGTH: 213

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_92739C.1.pap

US-10-437-963-196932

Query Match

Best Local Similarity 3.6%; Score 8; DB 4; Length 213;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 RQEEER 149

US-10-732-923-18430

RESULT 41

US-10-732-923-18430
; Sequence 18430, Application US/10732923
; Publication No. US20050108791A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 196724

LENGTH: 209

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(209)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_110996C.1.pap

US-10-425-115-196724

Query Match

Best Local Similarity 3.6%; Score 8; DB 4; Length 209;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 TKVSEAE 137

US-10-437-963-196932

RESULT 40

US-10-437-963-196932
; Sequence 196932, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 196932

LENGTH: 213

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_92739C.1.pap

US-10-437-963-196932

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/ GENERAL INFORMATION:
/ APPLICANT: Edgerton, Michael D
/ TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
/ FILE REFERENCE: 38-15(52796)C
/ CURRENT APPLICATION NUMBER: US/10/732,923
/ PRIOR FILING DATE: 2003-12-10
/ PRIOR APPLICATION NUMBER: 10/310,154
/ PRIOR FILING DATE: 2002-12-04
/ NUMBER OF SEQ ID NOS: 24149
/ SEQ ID NO 18430
/ LENGTH: 234
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-732-923-18430

Query Match
Best Local Similarity 3.6%; Score 8; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 QEEERKR 151
Db 190 QEEERKR 197

RESULT 42
US-10-437-963-138843
/ Sequence 138843, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 138843
/ LENGTH: 246
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_40194C.1.pep
US-10-437-963-138843

Query Match
Best Local Similarity 3.6%; Score 8; DB 4; Length 246;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 RROQEEER 148
Db 66 RROQEEER 73

RESULT 43
US-10-128-714-3119
/ Sequence 3119, Application US/10128714
/ Publication No. US20030119013A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Bo
/ APPLICANT: Hu, Wengqi
/ APPLICANT: Tishkoff, Daniel
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Eroszhkin, Alexey M
/ APPLICANT: Lemieux, Sebastien M
/ TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
/ TITLE OF INVENTION: Methods of Use
```

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/ FILE REFERENCE: 10182-018-999
/ CURRENT APPLICATION NUMBER: US/10/128,714
/ CURRENT FILING DATE: 2002-04-23
/ PRIOR APPLICATION NUMBER: US 60/285,697
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: US 60/287,066
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: US 60/295,890
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US 60/303,899
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/316,362
/ PRIOR FILING DATE: 2001-08-31
/ NUMBER OF SEQ ID NOS: 8603
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3119
/ LENGTH: 358
/ TYPE: PRT
/ ORGANISM: Aspergillus fumigatus
US-10-128-714-3119

Query Match
Best Local Similarity 3.6%; Score 8; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 EERRRRP 153
Db 258 EERRRRP 265

RESULT 44
US-10-437-963-140721
/ Sequence 140721, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 140721
/ LENGTH: 369
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_41894C.1.pep
US-10-437-963-140721

Query Match
Best Local Similarity 3.6%; Score 8; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 RROQEEER 148
Db 156 RROQEEER 163

RESULT 45
US-10-425-115-242617
/ Sequence 242617, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
```

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 242617
LENGTH: 382
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(382)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_152851C.1.pcp
US-10-425-115-242617

Query Match
Best Local Similarity 3.6%; Score 8; DB 4; Length 382;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 TKVSEAE 167
Db 303 TKVSEAE 310

RESULT 46
US-10-128-714-8119
Sequence 8119, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroskin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8119
LENGTH: 517
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-128-714-8119

Query Match
Best Local Similarity 3.6%; Score 8; DB 4; Length 517;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 EBERKRP 153
Db 417 EBERKRP 424

RESULT 47

US-11-097-143-16161
Sequence 16161, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637

Query Match
Best Local Similarity 3.6%; Score 8; DB 6; Length 547;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 OKTFTKW 50
Db 21 OKTFTKW 28

RESULT 48
US-11-097-143-16218
Sequence 16218, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16218
; LENGTH: 690
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-16218

Query Match 3.6%; Score 8; DB 6; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 EEEERKR 152
|||
DB 180 EEEERKR 187

RESULT 49
US-10-733-969A-5
; Sequence 5, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; APPLICANT: LIU, TONG HUA
; APPLICANT: LU, ZHAO HUI
; APPLICANT: SHEN, YAN
; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER
; FILE REFERENCE: 21525
; CURRENT APPLICATION NUMBER: US/10/733,969A
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 02026058.2
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Alpha-actinin 4; Accession NO: 043707
US-10-733-969A-5

Query Match 3.6%; Score 8; DB 5; Length 911;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 SGERLKP 90
|||
DB 92 SGERLKP 99

RESULT 50
US-10-369-18546
; Sequence 18546, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18546
; LENGTH: 1190

; TYPE: PRT
; ORGANISM: Halobacterium sp. NRC-1
US-10-369-18546

Query Match 3.6%; Score 8; DB 4; Length 1190;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 LQDEREAV 42
|||
DB 768 LQDEREAV 775

Search completed: March 4, 2006, 07:14:28
Job time : 181 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 4, 2006, 07:06:31 ; Search time 40 Seconds
(without alignments)
529.192 Million cell updates/sec

Title: US-10-695-994a-7

Perfect score: 220

Sequence: 1 MELORTSSISGPISPATYQ.....QNYKNFNSRTASHSMGSM 220

Scoring table: ~~Old~~
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word-size: 6

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : PIR_80:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	44.1	2364	1 A44159	spectrin beta-G ch
2	38	17.3	2128	2 I52577	beta-spectrin - mo
3	38	17.3	2137	1 SHUB	spectrin beta chai
4	27	12.3	2388	2 JEO271	beta spectrin, bet
5	19	8.6	2291	1 A46147	spectrin beta chai
6	17	7.7	30	2 S21195	spectrin beta chai
7	16	7.3	707	2 S28854	spectrin beta chai
8	14	6.4	2326	2 T28140	spectrin beta chai
9	11	5.0	41	2 I65645	hypothetical prote
10	11	5.0	101	2 F59404	Duchenne muscular
11	11	5.0	214	2 F59404	plectin isoform pl
12	11	5.0	385	2 S66292	actin-croslinking
13	11	5.0	964	2 D58404	plectin isoform pl
14	11	5.0	1355	2 T22552	hypothetical prote
15	11	5.0	1825	2 T42725	actin binding prot
16	11	5.0	1885	2 T30847	actin binding prot
17	11	5.0	3685	1 A27605	dytrophin, muscle
18	11	5.0	4574	2 G02520	plectin - human
19	10	4.5	2396	2 T13714	Kakapo gene protei
20	9	4.1	98	2 S06461	dytrophin, brain
21	9	4.1	230	2 J39161	dytrophin isoform 2
22	9	4.1	292	2 JEO233	dytrophin isoform 2
23	9	4.1	461	2 I39160	dytrophin-1 - scall
24	9	4.1	511	2 I49290	dytrophin isoform 1
25	9	4.1	602	2 C75120	hypothetical prote
26	9	4.1	686	2 I48298	dytrophin isoform 2
27	9	4.1	874	2 T15570	hypothetical prote
28	9	4.1	3433	1 S28381	utrophin - human
29	9	4.1	3660	1 S02041	dytrophin, muscle

30	9	4.1	3678	2 S28916	dytrophin - mouse
31	8	3.6	592	2 P86242	unknown protein, 9
32	8	3.6	894	1 PAHUA2	alpha-actinin 2 -
33	8	3.6	897	2 S02032	alpha-actinin 2, 8
34	8	3.6	904	2 S45673	alpha-actinin, 115
35	8	3.6	911	2 UC7186	alpha-actinin-4 -
36	8	3.6	1089	2 T36663	protein kinase, tr
37	8	3.6	1190	2 E84193	chromosome segrega
38	8	3.6	1645	2 A37792	spectrin beta-H ch
39	8	3.6	1846	2 T42047	insulin receptor h
40	8	3.6	2414	2 A54277	transcription adap
41	8	3.6	4063	2 T42993	probable spectrin
42	8	3.6	4101	2 T23630	hypothetical prote
43	7	3.2	125	2 I65646	Duchenne muscular
44	7	3.2	172	2 S56905	hypothetical prote
45	7	3.2	218	2 B84165	glucose-1-phosphat
46	7	3.2	226	2 T49719	hypothetical prote
47	7	3.2	251	2 AB0957	conserved hypotet
48	7	3.2	266	1 F69844	conserved hypotet
49	7	3.2	279	2 G97246	arac-type DNA-bind
50	7	3.2	290	2 G86155	hypothetical prote
51	7	3.2	291	2 A85017	hypothetical prote
52	7	3.2	292	2 AG2127	hypothetical prote
53	7	3.2	311	2 T35159	hypothetical prote
54	7	3.2	314	2 JC4951	tropomn T - scall
55	7	3.2	327	2 AH2368	hypothetical prote
56	7	3.2	356	2 S32147	natingenin 3-dioxy
57	7	3.2	357	2 S38338	natingenin 3-dioxy
58	7	3.2	357	2 S71772	natingenin 3-dioxy
59	7	3.2	357	2 S61415	natingenin 3-dioxy
60	7	3.2	357	2 A72220	conserved hypotet
61	7	3.2	358	2 T45755	flavanone 3-hydrox
62	7	3.2	360	2 S50830	Machado-Joseph dis
63	7	3.2	397	2 A11201	glycine betaine AB
64	7	3.2	397	2 AD1559	glycine betaine AB
65	7	3.2	408	2 S63528	phosphoglycerate k
66	7	3.2	412	2 T02725	probable serine/ch
67	7	3.2	413	1 S28602	translation releas
68	7	3.2	415	2 H80198	phosphoglycerate k
69	7	3.2	433	2 T24351	hypothetical prote
70	7	3.2	470	2 D85111	hypothetical prote
71	7	3.2	478	2 B90507	gamma-glutamyltran
72	7	3.2	481	2 S47441	transport prote in
73	7	3.2	498	1 S67859	Gumf protein - xan
74	7	3.2	515	2 T24781	hypothetical prote
75	7	3.2	520	2 T22971	hypothetical prote
76	7	3.2	538	2 S67766	RNA-export mediato
77	7	3.2	548	2 C75466	phytoene dehydroge
78	7	3.2	569	2 T02435	probable oxysterol
79	7	3.2	595	2 C82960	probable two-compo
80	7	3.2	621	1 T01935	natingenin 3-dioxy
81	7	3.2	633	2 E95937	probable mureindep
82	7	3.2	656	2 I49259	receptor interacti
83	7	3.2	669	2 C82984	ATP-dependent DNA
84	7	3.2	688	2 D72418	DNA ligase - Therm
85	7	3.2	701	2 H82978	guanosine-3',5'-bi
86	7	3.2	705	2 T01911	hypothetical prote
87	7	3.2	714	2 A70983	probable fusa2 pro
88	7	3.2	721	2 A39707	erythrocyte membra
89	7	3.2	755	2 H72262	sensor histidine k
90	7	3.2	764	1 S14113	1-phosphatidylinos
91	7	3.2	774	2 A24057	glycophorin-bindin
92	7	3.2	819	2 A13197	Tomb-dependent rec
93	7	3.2	822	2 S19947	fibroblast growth
94	7	3.2	822	2 B49151	potassium channel
95	7	3.2	828	2 T52046	penicillin binding
96	7	3.2	831	2 G82815	class I INCENP pro
97	7	3.2	839	2 T50590	bos23.5 protein -
98	7	3.2	848	2 S44732	hypothetical prote
99	7	3.2	854	2 T17288	gelation factor -
100	7	3.2	857	1 S05943	hypothetical prote
101	7	3.2	876	2 T19246	class II INCENP pr
102	7	3.2	877	2 I50591	

103	7	3.2	972	1	GNXSIV	genome polyprotein
104	7	3.2	972	2	T09624	genome polyprotein
105	7	3.2	1028	2	T01714	hypothetical prote
106	7	3.2	1069	2	T00377	KIA0642 protein -
107	7	3.2	1074	2	T01906	hypothetical prote
108	7	3.2	1091	2	C95133	exonuclease RexB
109	7	3.2	1091	2	G98001	second chain of ma
110	7	3.2	1106	2	S38783	integrin alpha cha
111	7	3.2	1135	2	I61867	alpha-7 integrin -
112	7	3.2	1142	2	T00022	BL20 protein - hum
113	7	3.2	1166	2	H71609	hypothetical prote
114	7	3.2	1254	2	A84818	myosin-VI [similar
115	7	3.2	1257	2	A88536	protein B0523.5 (I
116	7	3.2	1263	2	T15496	hypothetical prote
117	7	3.2	1265	2	A59299	unconventional myo
118	7	3.2	1336	2	S41794	SEC3 protein - yea
119	7	3.2	1407	1	S28589	trichothyalin - rab
120	7	3.2	1898	1	A45973	trichothyalin - hum
121	7	3.2	2440	2	S39162	transcription coac
122	7	3.2	2441	2	S39161	CRBB-binding prote
123	7	3.2	2962	2	T19756	hypothetical prote
124	7	3.2	4684	2	A59404	plectin [imported]
125	7	3.2	4687	1	A39638	plectin - rat
126	6	2.7	20	2	S33001	hypothetical prote
127	6	2.7	30	2	A44010	kit-ligand (altern
128	6	2.7	34	4	S78720	TYA protein YER138
129	6	2.7	34	4	S78704	TYA protein YBL107
130	6	2.7	37	2	A23617	conglutin delta-2
131	6	2.7	38	2	T70014	kallikrein - mouse
132	6	2.7	42	2	D47753	beta-defensin-13 -
133	6	2.7	44	2	T16453	hypothetical prote
134	6	2.7	48	2	T14966	hypothetical prote
135	6	2.7	52	2	AD1587	hypothetical prote
136	6	2.7	58	2	F69163	hypothetical prote
137	6	2.7	65	2	P89906	hypothetical prote
138	6	2.7	67	2	H90323	hypothetical prote
139	6	2.7	71	2	AF2766	hypothetical prote
140	6	2.7	80	2	S02067	glycerol kinase (B
141	6	2.7	81	2	E72650	hypothetical prote
142	6	2.7	91	2	T71950	serum amyloid A -
143	6	2.7	91	2	T37327	insulin homolog ce
144	6	2.7	93	2	B83263	hypothetical prote
145	6	2.7	94	2	AC1240	B. subtilis YlXr p
146	6	2.7	94	2	AG1602	B. subtilis YlXr p
147	6	2.7	95	2	T09383	vpr protein - huma
148	6	2.7	96	2	T01670	vpr protein - huma
149	6	2.7	96	2	T09444	vpr protein - huma
150	6	2.7	96	2	S54380	vpr protein - huma
151	6	2.7	97	1	D44001	intermediate filam
152	6	2.7	98	2	S44095	probable membrane
153	6	2.7	105	2	AE0408	cysteine proteinas
154	6	2.7	106	2	S13027	oryacystatin II -
155	6	2.7	107	2	A38375	exonuclease ABC C
156	6	2.7	110	2	A42573	conserved hypotet
157	6	2.7	111	2	B69117	conserved hypotet
158	6	2.7	113	2	C89828	hypothetical prote
159	6	2.7	117	2	A84147	hypothetical prote
160	6	2.7	118	2	B90178	hypothetical prote
161	6	2.7	119	2	F42523	A-ORF-A protein -
162	6	2.7	122	2	A23521	serum amyloid A3 p
163	6	2.7	122	2	A32807	replication termin
164	6	2.7	122	2	AG0321	conserved hypotet
165	6	2.7	123	2	T16234	hypothetical prote
166	6	2.7	125	2	T05609	hypothetical prote
167	6	2.7	127	2	PC2268	hypothetical prote
168	6	2.7	127	2	B83157	cytochrome P450 pr
169	6	2.7	131	2	B96566	hypothetical prote
170	6	2.7	131	2	S77840	hypothetical prote
171	6	2.7	134	2	B64062	probable leucine-t
172	6	2.7	134	2	E57233	opacity-associated
173	6	2.7	134	2	C57233	complexin II - hum
174	6	2.7	134	2	JC4426	complexin II - rat
175	6	2.7	134	2	D57233	synaphin - bovine
						complexin II - mou
176	6	2.7	136	2	G72670	probable ribosomal
177	6	2.7	139	2	G75127	hypothetical prote
178	6	2.7	139	2	E71003	hypothetical prote
179	6	2.7	141	2	G82188	hypothetical prote
180	6	2.7	142	2	T18098	dCMP deaminase hom
181	6	2.7	144	2	C71149	hypothetical prote
182	6	2.7	144	2	T18657	hypothetical prote
183	6	2.7	145	2	A87574	hypothetical prote
184	6	2.7	146	2	A97166	flagellar protein
185	6	2.7	145	2	S11398	pts fructose-speci
186	6	2.7	150	2	G64343	hypothetical prote
187	6	2.7	150	2	H87668	hypothetical prote
188	6	2.7	153	2	A33090	conglutin delta pr
189	6	2.7	159	2	H72613	hypothetical prote
190	6	2.7	161	2	D87406	ribosomal protein
191	6	2.7	164	2	T16168	hypothetical prote
192	6	2.7	165	2	F69819	conserved hypotet
193	6	2.7	167	1	F45390	trans-regulatory s
194	6	2.7	167	1	VKLJVA	trans-regulatory s
195	6	2.7	167	1	VKLJVS	trans-regulatory s
196	6	2.7	167	1	S65670	phosphoprotein pho
197	6	2.7	170	2	G87153	50S ribosomal prot
198	6	2.7	171	2	G58930	hypothetical prote
199	6	2.7	172	2	A75592	hypothetical prote
200	6	2.7	172	2	F85745	unknown protein en
201	6	2.7	173	2	T02332	probable Hmg-prote
202	6	2.7	176	2	S43463	mannose-binding le
203	6	2.7	176	2	F71803	hypothetical prote
204	6	2.7	176	2	D71336	probable peptidyl-
205	6	2.7	180	2	E70565	probable ribosomal
206	6	2.7	182	2	A83730	hypothetical prote
207	6	2.7	184	2	AG0736	hypothetical prote
208	6	2.7	184	2	F90873	probable antilelmi
209	6	2.7	185	2	C71899	hypothetical prote
210	6	2.7	185	2	AB3267	probable transcrip
211	6	2.7	190	2	AB2265	hypothetical prote
212	6	2.7	191	2	G69062	phenylacrylic acid
213	6	2.7	192	2	A55228	lme protein homolo
214	6	2.7	192	2	S17812	hypothetical prote
215	6	2.7	193	2	S32992	cellulium realsitan
216	6	2.7	193	2	H84531	hypothetical prote
217	6	2.7	193	2	AI2364	hypothetical prote
218	6	2.7	194	2	AI2364	dCMP deaminase (BC
219	6	2.7	195	1	A64050	delta large antige
220	6	2.7	195	1	SAV1DS	hypothetical prote
221	6	2.7	195	1	C97509	3'-phosphadenosin
222	6	2.7	196	2	C69839	hypothetical prote
223	6	2.7	197	2	B84272	hypothetical prote
224	6	2.7	198	1	R8ECFE	type 1 fibrinolyse
225	6	2.7	198	2	H91287	hypothetical prote
226	6	2.7	198	2	C86129	hypothetical prote
227	6	2.7	198	2	B64229	phosphoglucanate d
228	6	2.7	198	2	T15353	hypothetical prote
229	6	2.7	200	2	S07397	lipocalin - mouse
230	6	2.7	203	2	T50367	hypothetical prote
231	6	2.7	204	2	PS0262	DNA-directed RNA p
232	6	2.7	206	2	G70307	adenylate kinase (
233	6	2.7	208	2	AC1151	acyl-carrier prote
234	6	2.7	208	2	AD1510	acyl-carrier prote
235	6	2.7	212	2	T10230	hypothetical prote
236	6	2.7	212	2	UA0152	glycinin chain A7
237	6	2.7	213	2	T44588	probable transcrip
238	6	2.7	214	2	C64425	conserved hypotet
239	6	2.7	216	2	AI2395	GRF cyclonhydrolase
240	6	2.7	221	2	G70381	RNase III - Agutfe
241	6	2.7	221	2	C96918	hypothetical prote
242	6	2.7	223	2	S42679	GRF-binding protei
243	6	2.7	225	2	T36651	probable cation tr
244	6	2.7	226	2	D83875	hypothetical prote
245	6	2.7	227	2	B90429	nitroreductase, bl
246	6	2.7	229	2	S66342	ribonuclease II (B
247	6	2.7	229	2	G70073	two-component reas
248	6	2.7	229	2	C82141	cytidylate kinase

249	6	2.7	230	2	B83879	hypothetical prote
250	6	2.7	230	2	A75260	hypothetical prote
251	6	2.7	231	2	G81026	inositol monophosp
252	6	2.7	232	2	B63392	ABC transporter, h
253	6	2.7	232	2	T43754	hypothetical prote
254	6	2.7	233	1	WMBEHK	UL3 protein - huma
255	6	2.7	233	1	D69630	menaquinone biosyn
256	6	2.7	233	1	F69178	conserved hypothet
257	6	2.7	236	2	A10981	conserved hypothet
258	6	2.7	236	2	A75431	hypothetical prote
259	6	2.7	237	2	A99103	26S proteasome 10T
260	6	2.7	237	2	AE3619	transcription regu
261	6	2.7	238	1	QCBET4	US4 protein - huma
262	6	2.7	240	2	T03379	heat shock protein
263	6	2.7	240	2	G87345	glutathione S-tran
264	6	2.7	240	2	T41254	probable coactmer d
265	6	2.7	240	2	T24239	hypothetical prote
266	6	2.7	241	2	A87551	glutathione S-tran
267	6	2.7	241	2	S44893	ZK1236.7 protein -
268	6	2.7	241	2	S49014	lysin - lactococcu
269	6	2.7	241	2	C86492	hypothetical prote
270	6	2.7	241	2	S61925	cyst wall protein
271	6	2.7	241	2	C72130	hypothetical prote
272	6	2.7	242	2	T36929	hypothetical prote
273	6	2.7	243	2	T46221	PRE-MRNA SPLICING
274	6	2.7	244	2	S44822	FAAE2.3 protein -
275	6	2.7	246	2	T44624	chil protein (limp
276	6	2.7	246	2	T16403	hypothetical prote
277	6	2.7	247	2	A87174	hypothetical prote
278	6	2.7	247	2	T37001	hypothetical prote
279	6	2.7	249	2	AC0698	probable pathogeni
280	6	2.7	250	2	C64304	ABC transporter su
281	6	2.7	251	2	H75586	probable urea/short
282	6	2.7	252	1	S55047	indole-3-glycerol
283	6	2.7	252	2	B83584	probable molybdenu
284	6	2.7	252	2	T12795	hypothetical prote
285	6	2.7	252	2	A45594	ORF 5' of calmodul
286	6	2.7	253	1	A40582	type IV prepillin p
287	6	2.7	253	1	D82273	leader peptidase f
288	6	2.7	255	1	S04899	my-related protei
289	6	2.7	255	2	T36778	probable enoyl-(ac
290	6	2.7	256	2	A49156	acetyl-CoA carboxy
291	6	2.7	257	2	B83050	probable transcrip
292	6	2.7	257	2	T12092	G-box-binding prot
293	6	2.7	259	2	T21715	hypothetical prote
294	6	2.7	260	2	S11552	probable MASH-1 pr
295	6	2.7	261	2	T4532	hypothetical prote
296	6	2.7	264	2	D81971	glycinin A5A4B3 pr
297	6	2.7	268	2	P00199	dihydrodipicolinat
298	6	2.7	269	2	H84946	amino acid ABC tra
299	6	2.7	269	2	AF1737	hypothetical prote
300	6	2.7	269	2	C84241	pyruvate dehydroge
301	6	2.7	270	2	A13642	hypothetical prote
302	6	2.7	270	2	T22213	hypothetical prote
303	6	2.7	271	2	S67072	probable membrane
304	6	2.7	272	2	A54617	transcription fact
305	6	2.7	272	2	AF0595	conserved hypothet
306	6	2.7	276	2	S73649	triacylglycerol 1i
307	6	2.7	276	2	C86030	hypothetical prote
308	6	2.7	276	2	G91183	hypothetical prote
309	6	2.7	276	2	S47775	hypothetical prote
310	6	2.7	276	2	T33529	ylaf protein - Bac
311	6	2.7	281	2	H97124	hypothetical prote
312	6	2.7	283	2	G84861	hypothetical prote
313	6	2.7	284	2	D95109	conserved hypothet
314	6	2.7	285	2	S21562	hypothetical prote
315	6	2.7	285	2	G66875	hypothetical prote
316	6	2.7	286	2	S17548	alpha-actinin - ra
317	6	2.7	286	2	G65082	putative general s
318	6	2.7	287	1	PWBY	inorganic diphosph
319	6	2.7	287	1	PWYKL	hypothetical prote
320	6	2.7	287	2	T22325	hypothetical prote
321	6	2.7	287	2	D69536	hypothetical prote
322	6	2.7	287	2	T05338	hypothetical prote
323	6	2.7	288	2	F64448	methylylologen-red
324	6	2.7	288	2	S58219	ABA-inducible prot
325	6	2.7	288	2	H88109	protein T24E12.3 l
326	6	2.7	289	2	T03395	probable lipase -
327	6	2.7	290	2	S39854	trax protein - Str
328	6	2.7	290	2	JC2097	legumin type B alp
329	6	2.7	291	1	JH0489	phosphoribosylamin
330	6	2.7	291	2	S55291	phosphoribosylamin
331	6	2.7	291	2	S55292	phosphoribosylamin
332	6	2.7	291	2	S55293	phosphoribosylamin
333	6	2.7	291	2	H70678	hypothetical prote
334	6	2.7	291	2	AH1308	methylyltransferase
335	6	2.7	291	2	AH1680	methylyltransferase
336	6	2.7	291	2	S27721	hypothetical prote
337	6	2.7	291	2	T40277	probable membrane
338	6	2.7	294	2	S59774	conserved hypothet
339	6	2.7	297	2	G97977	beta-SNAP protein
340	6	2.7	298	2	S32368	peptidase, M23/M37
341	6	2.7	298	2	H87533	hypothetical prote
342	6	2.7	300	2	P90274	hypothetical prote
343	6	2.7	300	2	AC1924	hypothetical prote
344	6	2.7	301	2	B85087	probable phosphogl
345	6	2.7	302	2	A33964	regulatory protein
346	6	2.7	303	2	JC5140	urate oxidase (BC
347	6	2.7	303	2	T29321	hypothetical prote
348	6	2.7	303	2	S77235	hypothetical prote
349	6	2.7	305	2	E70410	hypothetical prote
350	6	2.7	307	2	T29222	hypothetical prote
351	6	2.7	307	2	AG2862	conserved hypothet
352	6	2.7	307	2	P97639	hypothetical prote
353	6	2.7	308	2	D71353	hypothetical prote
354	6	2.7	308	2	T46294	hypothetical prote
355	6	2.7	308	2	A29379	glycine-rich prote
356	6	2.7	310	2	T05733	ribosome-associate
357	6	2.7	310	2	T34962	hypothetical prote
358	6	2.7	310	2	AB2235	hypothetical prote
359	6	2.7	310	2	T46429	hypothetical prote
360	6	2.7	311	2	AF2064	hypothetical prote
361	6	2.7	311	2	F84923	pale cress protein
362	6	2.7	315	2	AH0897	probable carboxydr
363	6	2.7	315	2	S76267	hypothetical prote
364	6	2.7	315	2	T45039	methylethetrahydro
365	6	2.7	316	2	S58719	probable membrane
366	6	2.7	317	2	A11887	coproporphyrinogen
367	6	2.7	317	2	B37804	febr protein - Esc
368	6	2.7	317	2	F86901	hypothetical prote
369	6	2.7	317	2	JC2110	tropomyosin-relate
370	6	2.7	317	2	B87365	hypothetical prote
371	6	2.7	320	2	S78604	taurin-binding pro
372	6	2.7	320	2	C90681	taurine transport
373	6	2.7	320	2	G85531	lamin C - mouse (f
374	6	2.7	320	2	S18324	hypothetical prote
375	6	2.7	321	2	T47138	hypothetical prote
376	6	2.7	322	2	H69457	ornithine cyclodea
377	6	2.7	322	2	S75280	hypothetical prote
378	6	2.7	322	2	AE3047	conserved hypothet
379	6	2.7	323	2	E71168	hypothetical prote
380	6	2.7	324	2	T00939	hypothetical prote
381	6	2.7	325	2	D75466	phytone synthase
382	6	2.7	325	2	S23007	CAMP response elem
383	6	2.7	326	2	AD3211	CAMP response elem
384	6	2.7	327	1	RDVZAS	transcription regu
385	6	2.7	327	1	E98238	ribonucleoside-dip
386	6	2.7	327	2	S22299	CAMP response elem
387	6	2.7	328	2	A99416	alcohol dehydrogen
388	6	2.7	328	2	A35663	CAMP response elem
389	6	2.7	328	2	C90196	conserved hypothet
390	6	2.7	328	2	T48248	ABC transporter-1i
391	6	2.7	329	2	T42996	hypothetical prote
392	6	2.7	329	2	S07577	legumin storage pr
393	6	2.7	330	2	T01190	DNA-binding protei
394	6	2.7	332	2	H82340	gluconate utilizat

395	6	2.7	333	2	AD2608	aldo-keto reductas
396	6	2.7	333	2	JCS313	UDPglucose 4-epime
397	6	2.7	334	2	AB0643	DNA polymerase III
398	6	2.7	334	2	B81406	probable integral
399	6	2.7	335	2	S44224	scyllo-inosamine-4
400	6	2.7	335	2	S44227	amidotransferase
401	6	2.7	335	2	S07576	legumin storage pr
402	6	2.7	335	2	S07576	legumin storage pr
403	6	2.7	336	2	AB2973	probable transcript
404	6	2.7	337	2	S42416	probable membrane
405	6	2.7	338	2	B83861	hypothetical prote
406	6	2.7	340	2	C70030	hypothetical prote
407	6	2.7	340	2	A69420	hypothetical prote
408	6	2.7	341	2	S03343	CAMP response elem
409	6	2.7	343	2	H84000	spore photoproduct
410	6	2.7	345	2	AB1813	hypothetical prote
411	6	2.7	345	2	T37685	probable vanadate
412	6	2.7	346	2	D47211	GTP-binding protei
413	6	2.7	347	2	S50403	TF134 protein - ye
414	6	2.7	347	2	G95402	hypothetical prote
415	6	2.7	348	2	B69162	lipase modulator X
416	6	2.7	350	2	B82713	glucose-1-phosphat
417	6	2.7	352	2	S58687	phosphoribosyl tra
418	6	2.7	352	2	C84342	probable dtdp-1-gi
419	6	2.7	353	2	T46521	hypothetical prote
420	6	2.7	353	2	C72479	hypothetical prote
421	6	2.7	353	2	S69047	hypothetical prote
422	6	2.7	354	2	A86843	prephenate dehydro
423	6	2.7	354	2	S28765	hypothetical prote
424	6	2.7	354	2	G81939	hypothetical prote
425	6	2.7	355	2	I49339	macrophage inflamm
426	6	2.7	355	2	H96012	probable sugar upt
427	6	2.7	359	2	T48396	fructose-bisphosph
428	6	2.7	359	2	AH1145	conserved hypotet
429	6	2.7	359	2	T47770	hypothetical prote
430	6	2.7	360	2	T22576	hypothetical prote
431	6	2.7	360	2	T35374	probable regulator
432	6	2.7	360	2	AF3175	DNA-directed DNA p
433	6	2.7	360	2	JCS804	CDPglucose 4,6-deh
434	6	2.7	362	1	S61924	cyst wall protein
435	6	2.7	364	1	S77360	chid protein - Syn
436	6	2.7	364	1	S28771	polysialacturonase
437	6	2.7	364	2	AB2993	glycosyltransferas
438	6	2.7	365	2	H90113	nucleolar snRNP pr
439	6	2.7	366	2	T50453	probable glycosylt
440	6	2.7	366	2	G83460	hypothetical prote
441	6	2.7	367	2	H82307	conserved hypotet
442	6	2.7	368	2	D70481	glucosyl transfera
443	6	2.7	368	2	C29356	hydroxyproline-ric
444	6	2.7	369	2	C97390	aldo/keto reductas
445	6	2.7	370	2	H64480	hypothetical prote
446	6	2.7	370	2	JC7591	spinal cord-deriva
447	6	2.7	374	2	F87596	hypothetical prote
448	6	2.7	374	2	E95167	ABC transporter, A
449	6	2.7	375	2	H84666	probable MYB famiI
450	6	2.7	378	2	S38962	serpin - pig
451	6	2.7	378	2	G02313	CDC37 homolog - hu
452	6	2.7	379	2	T36831	probable two-compo
453	6	2.7	379	2	P96565	hypothetical prote
454	6	2.7	380	2	T48953	UDPglucose-hexose-
455	6	2.7	380	2	T48953	hypothetical prote
456	6	2.7	380	2	T26255	hypothetical prote
457	6	2.7	381	2	S65212	hypothetical prote
458	6	2.7	381	2	C84650	hypothetical prote
459	6	2.7	381	2	S69065	probable membrane
460	6	2.7	382	2	T15204	hypothetical prote
461	6	2.7	383	2	G84597	probable Xap-5 pro
462	6	2.7	383	2	C96581	hypothetical prote
463	6	2.7	385	1	RGBSDS	degradative enzyme
464	6	2.7	385	1	R83725	hypothetical prote
465	6	2.7	386	2	T02640	hypothetical prote
466	6	2.7	386	2	S37691	ran GTPase activat
467	6	2.7	386	2	T39461	hypothetical prote
468	6	2.7	387	2	AB2036	fatty oxidation co
469	6	2.7	387	2	H86445	probable G-Box bin
470	6	2.7	387	2	AD1960	two-component hydr
471	6	2.7	388	2	A42465	integrase - phage
472	6	2.7	388	2	T41089	hypothetical prote
473	6	2.7	389	2	T03612	chalcone synthase
474	6	2.7	389	2	T02970	hypothetical prote
475	6	2.7	389	2	C96830	unknown protein F1
476	6	2.7	389	2	T27085	hypothetical prote
477	6	2.7	390	1	W2MLRB	E2 protein - cotto
478	6	2.7	390	2	S65672	phosphoprotein pho
479	6	2.7	391	2	G89822	hypothetical prote
480	6	2.7	391	2	B64307	ammonium transport
481	6	2.7	393	2	A10319	probable 2-octapre
482	6	2.7	393	2	I49016	phosphoprotein pho
483	6	2.7	394	2	E71136	threonine synthase
484	6	2.7	394	2	J02041	polymerase-aseosia
485	6	2.7	394	2	B75439	conserved hypotet
486	6	2.7	395	2	B90546	phosphopentomutase
487	6	2.7	395	2	B75512	conserved hypotet
488	6	2.7	396	2	I75615	mammary tumor inte
489	6	2.7	397	2	S66700	probable membrane
490	6	2.7	398	2	H72257	hypothetical prote
491	6	2.7	398	2	AB0975	probable racemase
492	6	2.7	399	1	HMXRM2	sigma 1 protein -
493	6	2.7	399	2	G96690	unknown protein P2
494	6	2.7	399	2	B66289	TFEN1.7 protein -
495	6	2.7	400	2	C89955	hypothetical prote
496	6	2.7	400	2	H70405	conserved hypotet
497	6	2.7	401	2	D72386	threonine ammonia-
498	6	2.7	402	2	A72312	conserved hypotet
499	6	2.7	403	1	C69213	protein-export mem
500	6	2.7	404	2	AB1832	hypothetical prote
501	6	2.7	406	2	H87392	hypothetical prote
502	6	2.7	406	2	T24492	hypothetical prote
503	6	2.7	407	2	C64250	tyrosine-CRNA ligase
504	6	2.7	407	2	T14909	bZIP DNA-binding p
505	6	2.7	408	2	T31254	bZIP DNA-binding p
506	6	2.7	408	2	F85023	biphényl dioxygena
507	6	2.7	408	2	H98290	probable potassium
508	6	2.7	409	2	T11901	NADH2 dehydrogenas
509	6	2.7	411	2	C98142	hypothetical prote
510	6	2.7	413	2	H88481	protein let-756 (I
511	6	2.7	419	2	AD3246	P-450 monooxygenas
512	6	2.7	420	2	T14911	bZIP DNA-binding p
513	6	2.7	420	2	JC7229	vitamin D receptor
514	6	2.7	420	2	S43559	collided coil protei
515	6	2.7	420	2	S35301	rfbH protein - Yer
516	6	2.7	421	2	AH3627	maltose-binding pe
517	6	2.7	422	2	S35480	hypothetical prote
518	6	2.7	423	2	G95880	probable trehalose
519	6	2.7	423	2	AF3466	trehalose/maltose
520	6	2.7	424	2	AB1034	UV protection prot
521	6	2.7	424	2	B38176	samb protein - Sal
522	6	2.7	425	2	B64403	translacion releas
523	6	2.7	425	2	UC7230	vitamin D receptor
524	6	2.7	429	2	S67101	probable nicotinat
525	6	2.7	436	2	T51540	hypothetical prote
526	6	2.7	436	2	T14816	hypothetical prote
527	6	2.7	436	2	T15331	hypothetical prote
528	6	2.7	439	2	T49334	basic transcriptio
529	6	2.7	439	2	T31031	hypothetical prote
530	6	2.7	442	2	H69181	hypothetical prote
531	6	2.7	443	2	I39538	alpha-amyase - Ae
532	6	2.7	443	2	T47963	hypothetical prote
533	6	2.7	445	2	I40682	phosphoglucosate d
534	6	2.7	445	2	I40685	phosphoglucosate d
535	6	2.7	445	2	I40684	phosphoglucosate d
536	6	2.7	445	2	I40681	phosphoglucosate d
537	6	2.7	445	2	T31581	hypothetical prote
538	6	2.7	446	2	A33284	chromogranin A pre
539	6	2.7	447	2	AF2295	hypothetical prote
540	6	2.7	448	2	F95122	protein kinase, pr

541	6	2.7	449	2	C69086	614	6	2.7	517	2	T51328	transcription init
542	6	2.7	451	2	G82218	615	6	2.7	518	2	AB0843	glutamate-cysteine
543	6	2.7	452	2	S64211	616	6	2.7	519	2	B82932	spermidine/putresc
544	6	2.7	452	2	AT2966	617	6	2.7	520	1	G86662	2',3'-cyclic-nucle
545	6	2.7	452	2	B98316	618	6	2.7	521	1	T37252	probable matrix me
546	6	2.7	452	2	T22948	619	6	2.7	522	1	DEF66	glucose-6-phosphat
547	6	2.7	454	2	D98033	620	6	2.7	524	2	A47740	glucose-6-phosphat
548	6	2.7	455	2	AD1723	621	6	2.7	525	2	T31563	hypothetical prote
549	6	2.7	455	2	S33033	622	6	2.7	526	2	T07082	lycopene epsilon-c
550	6	2.7	457	2	S39079	623	6	2.7	526	2	UC7248	hypothetical prote
551	6	2.7	458	1	C70058	624	6	2.7	527	1	CSRT	alpha-N-acetylglata
552	6	2.7	459	2	B64171	625	6	2.7	527	2	A36695	catalase (EC 1.11.
553	6	2.7	462	1	A60746	626	6	2.7	527	2	P64210	hypothetical prote
554	6	2.7	462	2	I53414	627	6	2.7	530	1	S57907	carboxypeptidase D
555	6	2.7	462	2	C34829	628	6	2.7	530	1	G95279	probable ABC trans
556	6	2.7	464	2	G86566	629	6	2.7	531	2	S48087	t-complex-type mol
557	6	2.7	464	2	D72058	630	6	2.7	531	2	S43063	t-complex-type mol
558	6	2.7	465	2	T40697	631	6	2.7	531	2	B69346	signal-transducing
559	6	2.7	465	2	B70213	632	6	2.7	532	2	C87793	protein C27A12.3 [
560	6	2.7	468	2	I62463	633	6	2.7	534	2	T39903	serine-rich protei
561	6	2.7	468	2	T34679	634	6	2.7	535	2	S19729	xylian 1,4-beta-xy
562	6	2.7	468	2	G71231	635	6	2.7	537	2	T48599	hypothetical prote
563	6	2.7	469	2	S69640	636	6	2.7	538	1	T40151	hypothetical prote
564	6	2.7	470	2	T10193	637	6	2.7	538	2	B84759	hypothetical prote
565	6	2.7	470	2	T22785	638	6	2.7	539	2	T15943	t-complex protein
566	6	2.7	470	2	T29380	639	6	2.7	540	2	S21825	vicillin-like stora
567	6	2.7	471	2	T21102	640	6	2.7	541	2	S43061	t-complex-type mol
568	6	2.7	471	2	S66829	641	6	2.7	545	2	T05510	hypothetical prote
569	6	2.7	471	2	S41768	642	6	2.7	546	1	SYBYHM	histidine-tRNA lig
570	6	2.7	473	2	A54691	643	6	2.7	546	2	S6306	hypothetical prote
571	6	2.7	474	2	T16441	644	6	2.7	551	1	JC5225	dsRNA-activated pr
572	6	2.7	475	1	Z28BL7	645	6	2.7	552	1	G69652	endopeptidase Ia (
573	6	2.7	476	2	T03745	646	6	2.7	553	2	G83864	transcription regu
574	6	2.7	478	1	S73920	647	6	2.7	559	2	S52941	period protein (Cl
575	6	2.7	478	1	S60754	648	6	2.7	559	2	S52943	period protein (Cl
576	6	2.7	478	2	S69974	649	6	2.7	560	2	S11004	glycinn G4 precu
577	6	2.7	479	2	D86182	650	6	2.7	561	2	AF0629	cell invasion prot
578	6	2.7	481	2	B75167	651	6	2.7	562	1	FWSYCS	glycinn chain A5A
579	6	2.7	481	2	H70679	652	6	2.7	562	2	T33174	hypothetical prote
580	6	2.7	481	2	F71048	653	6	2.7	562	2	PC7084	hypothetical prote
581	6	2.7	481	2	S04605	654	6	2.7	562	2	S20946	GRP-binding protei
582	6	2.7	484	2	AG3184	655	6	2.7	562	2	T49788	glycinn G4 precu
583	6	2.7	484	2	AF3529	656	6	2.7	563	2	S54802	related to merzoi
584	6	2.7	484	2	S11003	657	6	2.7	566	2	S22477	glycinn A5AAB3 ch
585	6	2.7	484	2	A24942	658	6	2.7	566	2	A84485	vicillin precursor
586	6	2.7	486	1	TVHUEG	659	6	2.7	567	2	H84770	hypothetical prote
587	6	2.7	486	2	S74319	660	6	2.7	567	2	C69014	probable receptor-
588	6	2.7	488	2	T05313	661	6	2.7	569	2	F87501	oxaloacetate decar
589	6	2.7	488	2	C86183	662	6	2.7	569	2	S74053	hypothetical prote
590	6	2.7	492	2	A83632	663	6	2.7	571	2	T31170	probable acylamino
591	6	2.7	492	2	B72389	664	6	2.7	572	1	VBHUC	maturase-related p
592	6	2.7	494	2	T02523	665	6	2.7	573	2	A53234	lamin C - human
593	6	2.7	495	2	AB0636	666	6	2.7	574	2	S04333	globulin-1S, GLB1S
594	6	2.7	496	2	E88987	667	6	2.7	574	2	S48860	gene a17 protei
595	6	2.7	496	2	AD1211	668	6	2.7	575	2	G69834	transporter bindi
596	6	2.7	496	2	AD1567	669	6	2.7	577	2	D65073	single-stranded DN
597	6	2.7	498	2	C47021	670	6	2.7	577	2	D51099	sBDNA exonuclease
598	6	2.7	498	2	F83523	671	6	2.7	577	2	H85944	sBDNA exonuclease
599	6	2.7	499	1	Z2BP22	672	6	2.7	577	2	AD1440	hypothetical prote
600	6	2.7	499	2	F72768	673	6	2.7	577	2	S64250	probable membrane
601	6	2.7	499	2	F69833	674	6	2.7	578	2	S23847	hypothetical prote
602	6	2.7	501	2	T00213	675	6	2.7	578	2	G75632	probable oligopept
603	6	2.7	501	2	S22669	676	6	2.7	579	2	UT0494	alpha-glucosidase
604	6	2.7	501	2	I39360	677	6	2.7	579	2	JC7170	fibxin-1-like 71 K
605	6	2.7	506	2	F71513	678	6	2.7	580	2	T21493	hypothetical prote
606	6	2.7	506	2	C81704	679	6	2.7	581	2	T45889	erin - bovine
607	6	2.7	507	2	AH2717	680	6	2.7	582	2	B53234	vicillin-like stora
608	6	2.7	507	2	C97499	681	6	2.7	582	2	JC7285	GRP-binding protei
609	6	2.7	509	2	AB0683	682	6	2.7	584	2	T40500	2-isopropylmalate
610	6	2.7	512	1	G69170	683	6	2.7	584	2	S53902	regulatory protein
611	6	2.7	513	1	H89805	684	6	2.7	584	2	F75090	archaeosine trna-r
612	6	2.7	516	1	FMSYG3	685	6	2.7	586	1	A34400	erin [validated]
613	6	2.7	516	2	AD2279	686	6	2.7	590	2	B86440	probable protein k

687	6	2.7	590	2	P82686	phosphotransferase
688	6	2.7	591	2	T14364	probable transcrip
689	6	2.7	591	2	SS1303	hypothetical prote
690	6	2.7	599	2	D97818	nitrogen regulatio
691	6	2.7	600	2	T41165	hypothetical prote
692	6	2.7	600	2	T02692	hypothetical prote
693	6	2.7	601	2	G71666	nitrogen regulatio
694	6	2.7	604	2	G66993	hypothetical prote
695	6	2.7	605	2	AC1083	toxin components h
696	6	2.7	604	2	B87365	sensor histidine k
697	6	2.7	608	2	S72177	dextranase (EC 3.2
698	6	2.7	611	2	S65472	peptidyl-dipeptida
699	6	2.7	612	2	B81246	glutamine-fructose
700	6	2.7	612	2	T40936	probable leukotrie
701	6	2.7	615	2	AK3069	cold-shock dead-bo
702	6	2.7	616	2	P98217	inducible ATP-inde
703	6	2.7	615	2	A40595	methylmalonyl-CoA
704	6	2.7	619	2	A23872	2-isopropylmalate
705	6	2.7	619	2	D63194	PEP112-like protei
706	6	2.7	620	2	JH0821	95K golgi antigen
707	6	2.7	621	2	T48187	hypothetical prote
708	6	2.7	621	2	T37708	hypothetical prote
709	6	2.7	623	2	T40685	phosphatidylcholin
710	6	2.7	623	2	B82536	ABC transporter At
711	6	2.7	625	2	S86633	hypothetical prote
712	6	2.7	625	2	T32739	hypothetical prote
713	6	2.7	629	2	A29666	keratin, 65K type
714	6	2.7	630	2	T47177	hypothetical prote
715	6	2.7	633	2	H96748	unknown protein T1
716	6	2.7	634	2	B86293	T24D18.1 protein -
717	6	2.7	635	2	D64835	ABC-type transport
718	6	2.7	635	2	G85621	hypothetical prote
719	6	2.7	635	2	A10625	ABC transporter At
720	6	2.7	635	2	A90758	hypothetical prote
721	6	2.7	637	2	H96592	probable multispin
722	6	2.7	637	2	AB0173	ABC transporter At
723	6	2.7	639	2	G82194	ABC transporter, A
724	6	2.7	640	2	T08758	hypothetical prote
725	6	2.7	640	2	H83267	probable ATP-Bindl
726	6	2.7	642	1	S29320	fibrin - Yeast (S
727	6	2.7	645	2	A47081	triacylglycerol li
728	6	2.7	646	2	T47154	hypothetical prote
729	6	2.7	646	2	T38171	probable serine/ch
730	6	2.7	647	2	E64170	ABC-type transport
731	6	2.7	648	2	B40727	S-M checkpoint con
732	6	2.7	649	2	AF2866	methyl-accepting c
733	6	2.7	649	2	D85135	hypothetical prote
734	6	2.7	651	2	C69374	conserved hypothet
735	6	2.7	652	2	T28924	hypothetical prote
736	6	2.7	653	2	A82647	phage-related inte
737	6	2.7	657	2	B75484	glycosyl hydrolase
738	6	2.7	657	2	S05517	lamin - chicken
739	6	2.7	658	2	A11385	exonuclease ABC (
740	6	2.7	658	2	D84869	probable receptor
741	6	2.7	658	2	S68418	protein phosphatas
742	6	2.7	659	2	F70175	rep helicase, sing
743	6	2.7	659	2	S11736	resistance protein
744	6	2.7	659	2	S11737	resistance protein
745	6	2.7	659	2	D84633	probable multispin
746	6	2.7	662	2	AG0479	probable alpha-any
747	6	2.7	662	2	T18233	probable transcrip
748	6	2.7	664	1	VEH01A	lamin A - human
749	6	2.7	664	2	T24459	hypothetical prote
750	6	2.7	664	2	C84869	probable receptor
751	6	2.7	665	2	S27267	lamin A - rat
752	6	2.7	665	2	S02358	lamin A - African
753	6	2.7	665	2	S28182	lamin A - mouse
754	6	2.7	666	2	T03090	hypothetical prote
755	6	2.7	666	2	H96723	hypothetical prote
756	6	2.7	669	2	T28754	hypothetical prote
757	6	2.7	670	2	C97643	similar to mcpo ge
758	6	2.7	670	2	D96739	hypothetical prote
759	6	2.7	672	2	A41075	inositol-1,4,5-tri
760	6	2.7	677	1	A45264	system b(0,+) amln
761	6	2.7	678	2	G75524	translational elonga
762	6	2.7	683	1	A41785	system b(0,+) amln
763	6	2.7	683	2	D97011	sensory transducti
764	6	2.7	684	2	A6154	Abi substrate ena
765	6	2.7	685	1	SBP4	NAD+-protein ADP-r
766	6	2.7	685	1	EBBY52	suppressor 2 prote
767	6	2.7	687	1	BB949	beta-galactosidase
768	6	2.7	687	2	D96553	hypothetical prote
769	6	2.7	687	2	T29148	hypothetical prote
770	6	2.7	689	2	T08988	cadmium-transporti
771	6	2.7	693	2	C83821	glycyl-tRNA synthe
772	6	2.7	696	2	S39837	SKTS protein - Yea
773	6	2.7	699	2	EB4555	hypothetical prote
774	6	2.7	705	2	T49461	probable croi prot
775	6	2.7	708	2	A72264	polynucleotide pho
776	6	2.7	711	2	A85352	cadmium-transporti
777	6	2.7	712	2	C71419	hypothetical prote
778	6	2.7	716	2	S45262	NF-AT component -
779	6	2.7	716	2	B90738	probably ATP-depen
780	6	2.7	716	2	G85588	probable ATP-depen
781	6	2.7	716	2	G64816	probable ATP-depen
782	6	2.7	718	2	A83282	probable TonB-depe
783	6	2.7	718	2	JC5805	transcription fact
784	6	2.7	722	2	H96986	endo-1,4-beta gluc
785	6	2.7	723	2	C36963	cellulose synthase
786	6	2.7	723	2	T02477	hypothetical prote
787	6	2.7	724	2	A38747	phosphatidylinosit
788	6	2.7	729	2	T50989	hypothetical prote
789	6	2.7	734	2	S46765	hypothetical prote
790	6	2.7	737	2	T15597	hypothetical prote
791	6	2.7	737	2	S65758	nitrate reductase
792	6	2.7	739	2	E86434	protein F178.27 (
793	6	2.7	743	2	T26102	hypothetical prote
794	6	2.7	746	2	AC1883	nitrate reductase
795	6	2.7	749	2	S13518	transposase Tam3 -
796	6	2.7	749	2	T43370	oligonuclearyltran
797	6	2.7	749	2	S50095	splicing regulator
798	6	2.7	749	2	B87599	hypothetical prote
799	6	2.7	750	2	D86245	hypothetical prote
800	6	2.7	751	1	T29357	1-phosphatidylinos
801	6	2.7	751	2	T39338	oligosaccharyl tra
802	6	2.7	752	2	F69338	pyruvate, water di
803	6	2.7	753	2	F69338	excision repair pr
804	6	2.7	754	1	DBBYD4	Y146 protein - yea
805	6	2.7	754	2	S61113	hypothetical prote
806	6	2.7	755	2	T20320	MAP kinase kinase
807	6	2.7	756	2	T50298	finger protein Y1L
808	6	2.7	758	2	S46625	protein transport
809	6	2.7	759	2	T41295	hypothetical prote
810	6	2.7	760	2	G71417	hypothetical prote
811	6	2.7	761	2	B64449	hypothetical prote
812	6	2.7	763	2	B86454	hypothetical prote
813	6	2.7	764	2	C83513	hypothetical prote
814	6	2.7	765	2	S74598	hypothetical prote
815	6	2.7	769	2	T24949	hypothetical prote
816	6	2.7	771	2	AB7532	glucosylase (limo
817	6	2.7	775	2	T42200	hypothetical prote
818	6	2.7	777	2	I48100	ADAM 5 protein pre
819	6	2.7	783	2	T00354	hypothetical prote
820	6	2.7	786	2	S67060	probable membrane
821	6	2.7	790	2	T24354	hypothetical prote
822	6	2.7	792	2	D64229	leucine-cRNA 119a8
823	6	2.7	793	2	S73779	leucine-cRNA 119a8
824	6	2.7	794	2	S55527	mammary gland fact
825	6	2.7	798	2	T15336	hypothetical prote
826	6	2.7	798	2	H87271	TonB-dependent rec
827	6	2.7	799	2	AB4729	sex-determining pr
828	6	2.7	800	2	T26683	hypothetical prote
829	6	2.7	803	2	AD1282	leucyl-tRNA synthe
830	6	2.7	804	2	AH1653	leucyl-tRNA synthe
831	6	2.7	804	2	B89961	leucine-tRNA 119a8
832	6	2.7	805	2	D69650	protein P43G9.7 (1

833	6	2.7	805	2	T32377	906	6	2.7	925	2	T00334	hypothetical prote
834	6	2.7	806	2	F82899	907	6	2.7	926	2	T38948	hypothetical coile
835	6	2.7	807	2	A84060	908	6	2.7	929	2	F75622	hypothetical prote
836	6	2.7	807	2	E90523	909	6	2.7	950	2	D70204	exinuclease ABC c
837	6	2.7	812	2	E97831	910	6	2.7	951	2	T04492	protein kinase hom
838	6	2.7	814	2	B71675	911	6	2.7	952	2	T18837	hypothetical prote
839	6	2.7	814	2	T14608	912	6	2.7	962	2	C43274	N-methyl D-asparta
840	6	2.7	815	2	B82746	913	6	2.7	966	2	T30017	hypothetical prote
841	6	2.7	819	2	G81698	914	6	2.7	968	2	D87570	exinuclease ABC.
842	6	2.7	819	2	T41544	915	6	2.7	969	2	A70912	probable leus prot
843	6	2.7	819	2	T40527	916	6	2.7	970	2	S29069	inositol polyphosp
844	6	2.7	820	2	A86510	917	6	2.7	972	2	T10023	leucine-tRNA ligase
845	6	2.7	820	2	C72113	918	6	2.7	972	2	S67048	MR10 protein - ye
846	6	2.7	822	2	S70012	919	6	2.7	973	2	A85055	probable leucyl tr
847	6	2.7	823	2	B87348	920	6	2.7	974	2	AH3361	exinuclease ABC c
848	6	2.7	824	2	T10020	921	6	2.7	979	2	T40006	hypothetical prote
849	6	2.7	826	2	T46060	922	6	2.7	982	1	VCLJVS	env polypotein pr
850	6	2.7	826	2	T46061	923	6	2.7	983	1	A45390	env polypotein pr
851	6	2.7	828	2	AD2004	924	6	2.7	990	2	A86215	protein T6D22.8 (1
852	6	2.7	829	2	H86726	925	6	2.7	990	2	H88733	protein F32B10.3 (
853	6	2.7	829	2	D82430	926	6	2.7	1002	2	S54252	deep orange protei
854	6	2.7	831	2	T05265	927	6	2.7	1003	2	T13856	ker protein - fru
855	6	2.7	832	2	T49494	928	6	2.7	1004	2	A71617	SERA antigen/papal
856	6	2.7	833	2	H95029	929	6	2.7	1009	2	S44621	C50C3.2 protein -
857	6	2.7	833	2	C97901	930	6	2.7	1012	2	B90389	conserved hypothet
858	6	2.7	834	2	T42702	931	6	2.7	1016	2	T30990	period protein - C
859	6	2.7	834	2	S54563	932	6	2.7	1017	2	T15598	hypothetical prote
860	6	2.7	837	2	S30971	933	6	2.7	1017	2	T42384	inositol-1,4,5-tri
861	6	2.7	839	2	B96538	934	6	2.7	1018	2	T30986	period protein - C
862	6	2.7	841	2	I50428	935	6	2.7	1023	2	JC4013	major acidict nucle
863	6	2.7	845	2	AB3337	936	6	2.7	1028	2	A59253	myosin I beta - hu
864	6	2.7	847	2	G75270	937	6	2.7	1028	2	S37146	myosin I heavy cha
865	6	2.7	848	1	JC1351	938	6	2.7	1032	1	S53571	hypothetical prote
866	6	2.7	849	1	UC1350	939	6	2.7	1043	1	SUSEMM	serine proteinase
867	6	2.7	851	2	T12503	940	6	2.7	1056	2	JQ2277	sucrose-phosphate
868	6	2.7	851	2	T38173	941	6	2.7	1061	2	A12579	conserved hypothet
869	6	2.7	853	1	A41220	942	6	2.7	1061	2	H97361	hypothetical prote
870	6	2.7	855	2	A34810	943	6	2.7	1062	2	D96540	hypothetical prote
871	6	2.7	861	2	T00434	944	6	2.7	1070	2	C75506	hypothetical prote
872	6	2.7	862	1	FAD0A	945	6	2.7	1071	2	S44798	F09G8.5 protein -
873	6	2.7	862	2	T05941	946	6	2.7	1071	2	S48378	probable membrane
874	6	2.7	862	2	B82312	947	6	2.7	1075	2	T48805	hypothetical prote
875	6	2.7	863	2	A53034	948	6	2.7	1078	2	T30879	dynein heavy chain
876	6	2.7	872	2	AC2134	949	6	2.7	1084	2	T13173	RNA-directed DNA p
877	6	2.7	872	2	S49538	950	6	2.7	1085	2	S62516	hypothetical colle
878	6	2.7	877	2	S49197	951	6	2.7	1086	2	S74251	phosphorylase kina
879	6	2.7	883	2	S57653	952	6	2.7	1087	2	S58147	protein kinase - f
880	6	2.7	883	2	S49126	953	6	2.7	1092	2	T20117	hypothetical prote
881	6	2.7	889	2	S50934	954	6	2.7	1093	2	S74250	phosphorylase kina
882	6	2.7	891	2	T28828	955	6	2.7	1093	2	A31758	phosphorylase kina
883	6	2.7	892	2	T50985	956	6	2.7	1093	2	B40793	phosphorylase kina
884	6	2.7	893	2	G59431	957	6	2.7	1106	1	PFH0B	platelet-derived g
885	6	2.7	894	2	T26149	958	6	2.7	1107	2	S61667	probable membrane
886	6	2.7	895	1	PAF6FA	959	6	2.7	1118	2	S75309	hypothetical prote
887	6	2.7	895	2	T13414	960	6	2.7	1122	2	B26427	period clock prote
888	6	2.7	900	2	S66264	961	6	2.7	1127	2	A25018	circadian rhythm p
889	6	2.7	901	1	FAH0A3	962	6	2.7	1128	2	A49660	bud emergence prot
890	6	2.7	901	1	BVECCA	963	6	2.7	1137	2	JC5950	integrin alpha-7 c
891	6	2.7	901	2	AE0519	964	6	2.7	1151	2	T33777	hypothetical prote
892	6	2.7	901	2	F85492	965	6	2.7	1169	2	A64505	p15 homolog - Met
893	6	2.7	901	2	F90641	966	6	2.7	1173	2	T43527	sp8 protein - fls
894	6	2.7	904	2	A10069	967	6	2.7	1173	2	T30608	proteophosphoglyca
895	6	2.7	905	2	T00475	968	6	2.7	1174	2	A40853	potassium channel
896	6	2.7	907	2	T35748	969	6	2.7	1175	2	D35815	myosin heavy chain
897	6	2.7	909	2	G69599	970	6	2.7	1176	2	C35815	myosin heavy chain
898	6	2.7	910	2	A48403	971	6	2.7	1176	2	C26427	period clock prote
899	6	2.7	912	2	A54423	972	6	2.7	1178	2	S57535	probable membrane
900	6	2.7	918	2	A88188	973	6	2.7	1178	2	S78475	mannosylphosphoryl
901	6	2.7	919	2	F83257	974	6	2.7	1186	2	S72229	metoic recombinat
902	6	2.7	920	2	T26147	975	6	2.7	1191	2	T14154	serine/threonine p
903	6	2.7	920	2	T13413	976	6	2.7	1192	2	T17089	homodomain-intera
904	6	2.7	924	2	S06117	977	6	2.7	1201	2	A35815	myosin heavy chain
905	6	2.7	925	2	T33732	978	6	2.7	1201	2	B35815	myosin heavy chain

979	6	2.7	1206	2	D84542	probable chloropia
980	6	2.7	1208	2	T23467	hypothetical prote
981	6	2.7	1209	2	T46027	hypothetical prote
982	6	2.7	1215	2	C84848	hypothetical prote
983	6	2.7	1218	2	A26588	period clock prote
984	6	2.7	1218	2	A26427	period clock prote
985	6	2.7	1223	2	T15316	hypothetical prote
986	6	2.7	1239	2	T14905	glutamate receptor
987	6	2.7	1240	2	S52734	hypothetical prote
988	6	2.7	1250	1	B45219	N-methyl-D-asparta
989	6	2.7	1254	2	T47141	hypothetical prote
990	6	2.7	1258	2	A12155	WD-repeat protein
991	6	2.7	1265	2	T51314	probable CO-induce
992	6	2.7	1274	2	T04018	hypothetical prote
993	6	2.7	1274	2	T19508	hypothetical prote
994	6	2.7	1283	2	S52500	oxysterol-binding
995	6	2.7	1284	2	T40578	hypothetical prote
996	6	2.7	1286	2	B71413	hypothetical prote
997	6	2.7	1289	2	T84505	calcium-dependent
998	6	2.7	1291	2	T06692	hypothetical prote
999	6	2.7	1295	2	S60179	pol polypotein ho
1000	6	2.7	1313	2	A48467	myosin heavy chain

ALIGNMENTS

RESULT 1

A44159
Spectrin beta-G chain - human
N:Alternate names: beta-spectrin general isoform, beta G-spectrin
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A44159
R:Hu, R.U.; Watanabe, M.; Bennett, V.
J. Biol. Chem. 267, 18715-18722, 1992
A:Title: Characterization of human brain cDNA encoding the general isoform of beta-spectrin
A:Reference number: A44159; MUID:92406787; PMID:1527002
A:Accession: A44159
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2364 <HU>
A:Cross-references: UNIPROT:Q01082; UNIPARC:UPI000004EC67; GB:M96803; NID:9338442; PIDN:
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBI:P113399)
C:Genetics: GDB:SPTBN1
A:Gene: GDB:120386; OMIM:182790
A:Map position: 2p21-2p21
C:Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology; pleck
C:Keywords: actin binding; cytoskeleton; duplication; heterodimer; membrane protein
F:53-271/Domain: alpha-actinin actin-binding domain homology <ACT>
F:501-412/Domain: spectrin/dystrophin repeat homology <SP1>
F:1697-1803/Domain: spectrin/dystrophin repeat homology <SP2>
F:2196-2305/Domain: pleckstrin repeat homology <PLK>

Query Match 44.1%; Score 97; DB 1; Length 2364;

Best Local Similarity 100.0%; Pred. No. 2e-89; 0; Indels 0; Gaps 0;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 DERBAVOKKPTFMVNSHLARVSCRITDLYTDLRDGMILKLEVLISGERLPRTKGRMR 96
Db 50 DERBAVOKKPTFMVNSHLARVSCRITDLYTDLRDGMILKLEVLISGERLPRTKGRMR 109
QY 97 IHCLLENVDKALQFLKEORVHLENMGSHDIDVGNHRL 133
Db 110 IHCLLENVDKALQFLKEORVHLENMGSHDIDVGNHRL 146

RESULT 2
152577
beta-spectrin - mouse
C:Species: Mus sp. (mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
C:Accession: 152577
R:Bloom, M.L.; Birkenmeier, C.S.; Barker, J.E.
Blood 82, 2906-2914, 1993
A:Title: Complete nucleotide sequence of the murine erythroid beta-spectrin cDNA and the
A:Reference number: 152577; MUID:94033578; PMID:8219239
A:Accession: 152577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2128 <RES>
A:Cross-references: UNIPARC:UPI000023884; GB:S66283; NID:9440899; PIDN:AA828600.1; PID:
C:Genetics: Sptd-1
A:Gene: Sptd-1
A:Introns: 418/3; 1742/2
C:Superfamily: spectrin beta chain; alpha-actinin actin-binding domain homology; spectri
C:Keywords: actin binding
F:53-271/Domain: alpha-actinin actin-binding domain homology <ACT>
F:1187-1892/Domain: spectrin/dystrophin repeat homology <SPH>

Query Match 17.3%; Score 38; DB 2; Length 2128;

Best Local Similarity 100.0%; Pred. No. 1.2e-29;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

SCHUB
Spectrin beta chain - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A37064; A39346; J0554; A28777; A39885; B23659; B42872; B27016; A2514
R:Winkelmann, J.C.; Chang, J.G.; Tee, W.T.; Scarpa, A.L.; Marchesi, V.T.; Forget, B.G.
J. Biol. Chem. 265, 11827-11832, 1990
A:Title: Full-length sequence of the cDNA for human erythroid beta-spectrin.
A:Reference number: A37064; MUID:90307707; PMID:2195026
A:Accession: A37064
A:Molecule type: mRNA
A:Residues: 1-2137 <WIN>
A:Cross-references: UNIPROT:P11277; UNIPARC:UPI0000135DB5; GB:J05500
A:Note: the authors translated the codon GAG for residue 536 as Arg, CAC for residue 801
R:Gallagher, P.G.; Tee, W.T.; Costa, F.; Scarpa, A.; Bolvin, P.; Delannay, J.; Forget, B.
J. Biol. Chem. 266, 15154-15159, 1991
A:Title: A splice site mutation of the beta-spectrin gene causing exon skipping in hared
A:Reference number: A39346; MUID:91332035; PMID:1840591
A:Accession: A39346
A:Molecule type: DNA
A:Residues: 2002-2137 <GAL>
A:Cross-references: UNIPARC:UPI0000173DB5; GB:J05500
R:Yoon, S.H.; Kentros, C.G.; Prchal, J.T.
Gene 91, 297-302, 1990
A:Title: Identification of an unusual deletion within homologous repeats of human reticu
A:Reference number: J0554; MUID:91007291; PMID:1976574
A:Accession: J0554
A:Molecule type: mRNA
A:Residues: 928-957, 'NY', 960-982, 'L', 984-1030, 'D', 1032-1755 <YOO>
A:Cross-references: UNIPARC:UPI0000173DB6; GB:M57948
R:Winkelmann, J.C.; Lecco, T.L.; Watkins, P.C.; Eddy, R.; Shows, T.B.; Linnebach, A.J.;
Blood 72, 328-334, 1988
A:Title: Molecular cloning of the cDNA for human erythrocyte beta-spectrin.
A:Reference number: A90733; MUID:88269838; PMID:3390609
A:Accession: A28777
A:Molecule type: mRNA
A:Residues: 1334-1373, 'R', 1375-1432; 1909-2137 <W12>
A:Cross-references: UNIPARC:UPI000016A607; UNIPARC:UPI000016A608; GB:J05500
A:Note: authors Yoon et al. show His to be the predominant residue at position 1374 and
R:Prchal, J.T.; Morley, B.J.; Yoon, S.H.; Coetzee, T.L.; Palek, J.; Conboy, J.G.; Kan, Y.
Proc. Natl. Acad. Sci. U.S.A. 84, 7468-7472, 1987
A:Title: Isolation and characterization of cDNA clones for human erythrocyte beta-spectr
A:Reference number: A39885; MUID:88041127; PMID:3478706
A:Accession: A39885

A/Molecule type: mRNA
 A/Residues: 1209-1482 <PRC>
 A/Cross-references: UNIPARC:UPI000016B05C; GB:M18054; NID:G338333; PIDN:AAA60572.1; PID:
 A/Experimental source: reticulocyte
 R.Winkelmann, J.C.; Costa, F.F.; Linzie, B.L.; Forget, B.G.
 J. Biol. Chem. 265, 20449-20454, 1990
 A/Title: Beta spectrin in human skeletal muscle. Tissue-specific differential processing
 A/Reference number: A23659; MUID:91056094; PMID:2243099
 A/Accession: B23659
 A/Molecule type: mRNA
 A/Residues: 2105-2137 <M13>
 A/Cross-references: UNIPARC:UPI0000173DB7; GB:M37885
 R.Speicher, D.W.; Weglarz, L.; Desilva, T.M.
 J. Biol. Chem. 267, 14775-14782, 1992
 A/Title: Properties of human red cell spectrin heterodimer (side-to-side) assembly and
 A/Reference number: A42872; MUID:92340516; PMID:1634521
 A/Accession: B42872
 A/Molecule type: Protein
 A/Residues: 47-56; 293-302; 1837-1846 <SP2>
 A/Cross-references: UNIPARC:UPI0000173DB8; UNIPARC:UPI0000173DB9; UNIPARC:UPI0000173DBA
 R.Speicher, D.W.; Marchesi, V.T.
 Nature 311, 177-180, 1984
 A/Title: Erythrocyte spectrin is comprised of many homologous triple helical segments.
 A/Reference number: A93341; MUID:84295638; PMID:6472478
 A/Accession: B27016
 A/Molecule type: Protein
 A/Residues: 292-324, 'X', 326-329, 'Y', 331-332; 434-532; 718-734, 'V', 736-773, 'X', 775-777; 1036
 1994-1997 <SPB>
 A/Cross-references: UNIPARC:UPI0000173DBB; UNIPARC:UPI0000173DBC; UNIPARC:UPI0000173DBD;
 A/Notes: The purified protein had a blocked amino end
 C/Comment: Spectrin is a major structural component of the erythrocyte membrane cytoskel
 C/Genetics:
 A/Gene: GDB:SPTB
 A/Cross-references: GDB:119602; OMIM:182870
 A/Map position: 14q23-14q23
 C/Superfamily: spectrin beta chain; alpha-actinin actin-binding domain homology; spectri
 C/Keywords: actin binding; cytoskeleton; duplication; erythrocyte; heterodimer; membrane
 F:53-271/Domain: alpha-actinin actin-binding domain homology <ACT>
 F:301-412/Domain: spectrin/dystrophin repeat homology <SP01>
 F:421-526/Domain: spectrin/dystrophin repeat homology <SP02>
 F:527-633/Domain: spectrin/dystrophin repeat homology <SP03>
 F:636-741/Domain: spectrin/dystrophin repeat homology <SP04>
 F:742-846/Domain: spectrin/dystrophin repeat homology <SP05>
 F:847-952/Domain: spectrin/dystrophin repeat homology <SP06>
 F:953-1059/Domain: spectrin/dystrophin repeat homology <SP07>
 F:1060-1166/Domain: spectrin/dystrophin repeat homology <SP08>
 F:1167-1272/Domain: spectrin/dystrophin repeat homology <SP09>
 F:1273-1377/Domain: spectrin/dystrophin repeat homology <SP10>
 F:1378-1476/Domain: spectrin/dystrophin repeat homology <SP11>
 F:1477-1582/Domain: spectrin/dystrophin repeat homology <SP12>
 F:1583-1688/Domain: spectrin/dystrophin repeat homology <SP13>
 F:1689-1795/Domain: spectrin/dystrophin repeat homology <SP14>
 F:1796-1901/Domain: spectrin/dystrophin repeat homology <SP15>
 F:1902-2007/Domain: spectrin/dystrophin repeat homology <SP16>
 F:2008-2118/Domain: spectrin/dystrophin repeat homology <SP17>
 Query Match 17.3%; Score 38; DB 1; Length 2137;
 Best Local Similarity 100.0%; Pred. No. 1.2e-29;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 95 MRHCLENVKALQFLKEORVHLNMGSHDIVDGNHRL 132
 DB 108 MRHCLENVKALQFLKEORVHLNMGSHDIVDGNHRL 145
 RESULT 4
 J80271
 beta spectrin, beta SpIII sigma1 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
 C/Accession: J80271
 R.Sakaguchi, G.; Orita, S.; Naito, A.; Maeda, M.; Igarashi, H.; Sasaki, T.; Takai, Y.
 Biochem. Biophys. Res. Commun. 248, 846-851, 1998

A/Title: A novel brain-specific isoform of beta spectrin: Isolation and its interaction
 A/Reference number: J80271; MUID:98369639; PMID:9704016
 A/Accession: J80271
 A/Molecule type: mRNA
 A/Residues: 1-238 <SAK>
 A/Cross-references: UNIPROT:Q9Q0N8; UNIPARC:UPI0000167BA0; DDBJ:AB00134
 A/Experimental source: brain
 C/Comment: This protein is especially expressed in brain, where it was enriched in the s
 C/Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology <ACT>
 F:304-415/Domain: spectrin/dystrophin repeat homology <SPH>
 Query Match 12.3%; Score 27; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 87 LKPTGMRHICLENVDKALQFLKEQ 113
 DB 103 LKPTGMRHICLENVDKALQFLKEQ 129
 RESULT 5
 A6147
 spectrin beta chain - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A6147; A33657
 R.Bjers, T.J.; Brantton, E.; Lue, R.A.; Whitograd, E.; Brantton, D.
 Proc. Natl. Acad. Sci. U.S.A. 89, 6187-6191, 1992
 A/Title: The complete sequence of Drosophila beta-spectrin reveals supra-motifs compris
 A/Reference number: A46147; MUID:92335263; PMID:1631106
 A/Accession: A46147
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-2291 <BE>
 A/Cross-references: UNIPROT:Q00963; UNIPARC:UPI000016B0B; GB:M92288; NID:G157019; PIDN:
 A/Notes: sequence extracted from NCBI backbone (NCBI:108607)
 R.Bjers, T.J.; Huesin-Chishti, A.; Dubreuil, R.R.; Brantton, D.; Goldstein, L.S.B.
 J. Cell Biol. 109, 1633-1641, 1989
 A/Title: Sequence similarity of the amino-terminal domain of Drosophila beta spectrin to
 A/Reference number: A33657; MUID:90009037; PMID:2671025
 A/Accession: A33657
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-800 <BY2>
 A/Cross-references: UNIPARC:UPI0000173DC2; GB:M92288
 C/Genetics:
 A/Gene: FlyBase:beta-Spec
 A/Cross-references: FlyBase:FBgn0003471
 C/Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology; pleck
 C/Keywords: actin binding; cytoskeleton
 F:49-267/Domain: alpha-actinin actin-binding domain homology <ACT>
 F:297-408/Domain: spectrin/dystrophin repeat homology <SP1>
 F:411-522/Domain: spectrin/dystrophin repeat homology <SP2>
 F:1638-1804/Domain: spectrin/dystrophin repeat homology <SP3>
 F:2146-2257/Domain: spectrin/dystrophin repeat homology <PLK>
 Query Match 8.6%; Score 19; DB 1; Length 2291;
 Best Local Similarity 100.0%; Pred. No. 2.4e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 75 LKLELVSGERLKPPTG 93
 DB 84 LKLELVSGERLKPPTG 102
 RESULT 6
 S21195
 spectrin beta chain - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
 C/Accession: S21195
 R.Fraplet, T.; Derancourt, J.; Pradel, L.A.

Eur. J. Biochem. 205, 85-91, 1992
A>Title: Actin and neurofilament binding domain of brain spectrin beta subunit.
A:Reference number: S21195; MUID:92209538; PMID:1555607
A:Accession: S21195
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-30 <PRA>
A:Cross-references: UNIPROT:Q9TMS2; UNIPARC:UPI000017768F
C:Superfamily: alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat H

Query Match 7.7%; Score 17; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 DERNAVOKKFTKWNVS 53
|||
Db 4 DERNAVOKKFTKWNVS 20

RESULT 7
S29854
spectrin beta chain - dog (fragment)
N:Alternate names: beta-spectrin
C:Species: Canis lupus familiaris (dog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S29854
R:Tan, S.; Shankar, V.; Gilmore, M.S.; Sachdev, G.P.
Biochim. Biophys. Acta 1172, 217-219, 1993
A>Title: Nucleotide sequence of a cDNA for canine beta-spectrin reveals high evolutionary
A:Reference number: S29854; MUID:93176817; PMID:8439565
A:Accession: S29854
A:Molecule type: mRNA
A:Residues: 1-707 <TRAN>
A:Cross-references: UNIPROT:Q28297; UNIPARC:UPI000087662; EMBL:L02897; NID:G164035; PID:
C:Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology; pleck
C:Keywords: actin binding; cytoskeleton; heterodimer; membrane protein
F:40-146/Domain: spectrin/dystrophin repeat homology <SP1>
F:253-358/Domain: spectrin/dystrophin repeat homology <SP2>
F:539-648/Domain: pleckstrin repeat homology <PLK>

Query Match 7.3%; Score 16; DB 2; Length 707;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RROQEEERKRPPSP 156
|||
Db 431 RROQEEERKRPPSP 446

RESULT 8
T29140
hypothetical protein K11C4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T29140
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid K11C4.
A:Reference number: Z20577
A:Accession: T29140
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2326 <PAU>
A:Cross-references: UNIPARC:UPI00000588F; EMBL:U64854; PIDN:AA018316.1; GSPDB:GN00023;
C:Genetics:
A:Experimental source: strain Bristol N2; clone K11C4
A:Gene: CESP:K11C4.3
A:Map position: 5
A:Introns: 105/1; 131/3; 155/3; 449/3; 2075/1; 2140/3; 2182/1; 2232/2; 2309/1
C:Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology; pleck

Query Match 6.4%; Score 14; DB 2; Length 2326;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWNVSHL 55
|||
Db 110 VOKKFTKWNVSHL 123

RESULT 9
165645
Duchenne muscular dystrophy protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 13-Aug-1999
C:Accession: 165645
R:Chelly, J.; Gilekhrantz, H.; Lambert, M.; Hamard, G.; Chafey, P.; Recan, D.; Katz, P.
Cell 63, 1239-1248, 1990
A>Title: Effect of dystrophin gene deletions on mRNA levels and processing in Duchenne a
A:Reference number: 152806; MUID:91084852; PMID:2261642
A:Accession: 165645
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-41 <RES>
A:Cross-references: UNIPARC:UPI000011F81C; GB:M63074; NID:G181589; PIDN:AAA52314.1; PID:
C:Genetics:
A:Gene: GDB:DMD
A:Cross-references: GDB:119850; OMIM:310200
A:Map position: Xp21.2-Xp21.2
C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrop
C:Keywords: muscular dystrophy

Query Match 5.0%; Score 11; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWNV 52
|||
Db 16 VOKKFTKWNV 26

RESULT 10
165644
Duchenne muscular dystrophy protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: 165644
R:Chelly, J.; Gilekhrantz, H.; Lambert, M.; Hamard, G.; Chafey, P.; Recan, D.; Katz, P.
Cell 63, 1239-1248, 1990
A>Title: Effect of dystrophin gene deletions on mRNA levels and processing in Duchenne a
A:Reference number: 152806; MUID:91084852; PMID:2261642
A:Accession: 165644
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-101 <RES>
A:Cross-references: UNIPROT:Q14172; UNIPARC:UPI000006E255; GB:M63073; NID:G181587; PIDN:
C:Genetics:
A:Gene: GDB:DMD
A:Cross-references: GDB:119850; OMIM:310200
A:Map position: Xp21.2-Xp21.2
C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrop
C:Keywords: muscular dystrophy

Query Match 5.0%; Score 11; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTKWNV 52
|||
Db 16 VOKKFTKWNV 26

RESULT 11
F59404
plectin isoform plect 1 (imported) - mouse
C:Species: Mus musculus (house mouse)

CjDate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 17-May-2002
CjAccession: F59404
RjFuchs, P.; Zorer, M.; Reznicek, G.A.; Spazierer, D.; Oehler, S.; Castanon, M.J.; Haug
Hum. Mol. Genet. 8: 2461-2472, 1999
A>Title: Unusual 5' transcript complexity of plectin isoforms: novel tissue-specific exc
A|Reference number: F59404; MUID:20025755; PMID:10556294
A|Accession: F59404
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-214 <STO>
A|Cross-references: UNIPARC:UPI000016C902; GB:AAFI8069; NID:g6578737; PIDN:AAFI8069.1
C|Superfamily: rat ribosomal protein S10; ribosomal protein S10 homology

Query Match: 5.0%; Score 11; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 42 VOKKFTKWN 52
Db 186 VOKKFTKWN 196

RESULT 12
S66292
actin-crosslinking protein ACF7 - human (fragment)
C|Species: Homo sapiens (man)
CjDate: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
CjAccession: S66292; S66291
RjByers, T.J.; Beggs, A.H.; McNally, E.M.; Kunkel, L.M.
Submitted to the EMBL Data Library, June 1995
A|Description: Novel actin crosslinker superfamily member identified by a two step deger
A|Reference number: S66292
A|Accession: S66292
A|Molecule type: DNA
A|Residues: 1-385 <BYE>
A|Cross-references: UNIPARC:UPI000070CP4; EMBL:L40626; NID:g845507; PID
RjByers, T.J.; Beggs, A.H.; McNally, E.M.; Kunkel, L.M.
FBS Lett. 368, 500-504, 1995
A>Title: Novel actin crosslinker superfamily member identified by a two step degenerate
A|Reference number: S66291; MUID:95361933; PMID:7635207
A|Accession: S66291
A|Status: nucleic acid sequence not shown
A|Molecule type: DNA
A|Residues: 97-309 <BYW>
A|Cross-references: UNIPARC:UPI0000177DB4; EMBL:L40626
C|Genetics:
A|Gene: GDB:ACF7
A|Cross-references: GDB:1323194
A|Map position: 1pter-1qter
C|Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
Fj94-308/Domain: alpha-actinin actin-binding domain homology <ACT>

Query Match: 5.0%; Score 11; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 42 VOKKFTKWN 52
Db 96 VOKKFTKWN 106

RESULT 13
D59404
plectin isoform plectin 1, alpha [imported] - mouse
C|Species: Mus musculus (house mouse)
CjDate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
CjAccession: D59404
RjFuchs, P.; Zorer, M.; Reznicek, G.A.; Spazierer, D.; Oehler, S.; Castanon, M.J.; Haug
Hum. Mol. Genet. 8: 2461-2472, 1999
A>Title: Unusual 5' transcript complexity of plectin isoforms: novel tissue-specific exc
A|Reference number: D59404; MUID:20025755; PMID:10556294
A|Accession: D59404
A|Status: preliminary

A|Molecule type: DNA
A|Residues: 1-964 <STO>
A|Cross-references: UNIPARC:UPI0000021F4E; GB:AAFI8068; NID:g6578735; PIDN:AAFI8068.1

Query Match: 5.0%; Score 11; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 42 VOKKFTKWN 52
Db 186 VOKKFTKWN 196

RESULT 14
T22552
hypothetical protein ZK1151.1 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
CjAccession: T22552; T27703
RjHarris, B.
Submitted to the EMBL Data Library, March 1997
A|Reference number: Z19580
A|Accession: T22552
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1355 <WIL>
A|Cross-references: UNIPARC:UPI000017BCEF; EMBL:Z92788; PIDN:CAB07214.1; GSPDB:GN00019;
A|Experimental source: clone F51B8
RjHarris, B.
Submitted to the EMBL Data Library, March 1997
A|Reference number: Z20408
A|Accession: T27703
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1355 <W12>
A|Cross-references: UNIPARC:UPI000017BCEF; EMBL:Z93398; PIDN:CAB07224.1; GSPDB:GN00019;
A|Experimental source: clone ZK1151
C|Genetics:
A|Gene: CESP:ZK1151.1
A|Map position: 1
A|Introns: 94/3; 124/3; 150/3; 209/3; 248/3; 311/3; 424/3; 734/2; 934/2; 1104/3; 1167/3;

Query Match: 5.0%; Score 11; DB 2; Length 1355;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 42 VOKKFTKWN 52
Db 79 VOKKFTKWN 89

RESULT 15
T42725
actin binding protein ACF7, neural isoform 1 - mouse (fragment)
C|Species: Mus musculus (house mouse)
CjDate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 03-Nov-2000
CjAccession: T42725
RjBernier, G.; Machieu, M.; De Repentigny, Y.; Vidal, S.M.; Kothary, R.
Genomics 38, 19-29, 1996
A>Title: Cloning and characterization of mouse ACF7, a novel member of the dystonin subf.
A|Reference number: Z20900; MUID:97124842; PMID:8994775
A|Accession: T42725
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-1825 <BER>
A|Cross-references: UNIPARC:UPI000016D118; EMBL:U67203; NID:g1675221; PID:g1675222; PIDN
C|Genetics:
A|Gene: ACF7
A|Map position: 4
C|Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
C|Keywords: actin binding

Query Match: 5.0%; Score 11; DB 2; Length 1825;

Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKVNN 52
|||||
22 VOKKFTTKVNN 32

Db 22 VOKKFTTKVNN 32

RESULT 16
T30847
actin binding protein ACF7, neural isoform 2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
R:Accession: T30847
R:Bernier, G.; Mathieu, M.; De Repentigny, Y.; Vidal, S.M.; Kochary, R.
Genomics 38, 19-29, 1996
A>Title: Cloning and characterization of mouse ACF7, a novel member of the dystonin subf
A:Reference number: Z20900; MUID:97124842; PMID:8954775
A:Accession: T30847
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1885 <BER>
A:Cross-references: UNIPARC:UPI000016D119; EMBL:U67204; NID:g1675223; PID:g1675224; PIDN
C:Genetics: mACF7
A:Gene: mACF7
A:Map position: 4
C:Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

Query Match 5.0%; Score 11; DB 2; Length 1885;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKVNN 52
|||||
82 VOKKFTTKVNN 92

Db 82 VOKKFTTKVNN 92

RESULT 17
A27605
dystrophin, muscle - human
N:Alternate names: Duchenne muscular dystrophy protein
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988 #sequence_revision 27-Jun-1994 #text_change 31-Dec-2004
C:Accession: A27605; S07710; A27162; S05291; A40134; S06051; S10346; S02243; S02242; S02
R:Koenig, M.; Monaco, A.P.; Kunkel, L.M.
Cell 53, 219-228, 1988
A>Title: The complete sequence of dystrophin predicts a rod-shaped cytoskeletal protein.
A:Reference number: A27605; MUID:88194521; PMID:3282674
A:Accession: A27605
A:Molecule type: mRNA
A:Residues: 1-3665 <KOE>
A:Cross-references: UNIPROT:Q14205; UNIPARC:UPI0000074045; GB:M18533; NID:g30823; PIDN:CA31453.1; PID
R:Rosenblatt, A.; Speer, A.; Billwiltz, H.; Cross, G.S.; Forrest, S.M.; Davies, K.E.
Nucleic Acids Res. 17, 5391, 1989
A>Title: Two human cDNA molecules coding for the Duchenne muscular dystrophy (DMD) locus
A:Reference number: S07710; MUID:89345106; PMID:2668885
A:Accession: S07710
A:Status: preliminary; translation not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132; 'P', 134-622; 'I', 624-783; 'G', 785-1196; 'F', 1198-1376; 'N', 1378-1468; 'Q', 1
A:Cross-references: UNIPARC:UPI000016A83D; EMBL:X14298; NID:g30845; PIDN:CAA2479.1; PID
A>Note: This sequence was submitted to the EMBL Data Library, February 1989
R:Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.
Cell 50, 509-517, 1987
A>Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary
A:Reference number: A90897; MUID:87273512; PMID:3607877
A:Accession: A27162
A:Molecule type: mRNA
A:Residues: 1-497 <KO2>
A:Cross-references: UNIPARC:UPI0000173E6D; GB:M18533
R:Cross, G.S.; Speer, A.; Rosenblatt, A.; Forrest, S.M.; Smith, T.J.; Edwards, Y.; Flint,
EMBO J. 6, 3277-3283, 1987
A>Title: Deletions of fetal and adult muscle cDNA in Duchenne and Becker muscular dystro

A:Reference number: S01263; MUID:88111512; PMID:3428261
A:Accession: S05291
A:Molecule type: mRNA
A:Residues: 404-556; 'T', 558-610; 'K', 612-622; 'I', 624-664; 'M', 665-783; 'G', 785-1137; 'P', 1139-1140
A:Cross-references: UNIPARC:UPI0000173E6C; EMBL:X06178
A>Note: 475-116 and 529-610 were also found
R:Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.
Science 238, 347-350, 1987
A>Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.
A:Reference number: A40134; MUID:88018015; PMID:3659917
A:Accession: A40134
A:Molecule type: mRNA
A:Residues: 451-1207 <HOF>
A:Cross-references: UNIPARC:UPI0000173E6D; GB:M18533
R:Blonden, L.A.J.; den Dunnen, J.T.; van Paassen, H.M.B.; Wapenaar, M.C.; Grootscholten,
Nucleic Acids Res. 17, 5611-5621, 1989
A>Title: High resolution deletion breakpoint mapping in the DMD gene by whole cosmid hyb
A:Reference number: S06051; MUID:89345155; PMID:2569720
A:Accession: S06051
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 2147-2204 <BLO>
A:Cross-references: UNIPARC:UPI000016A837; EMBL:X15495; NID:g30829; PIDN:CAA33518.1; PID
R:Speer, A.; Billwiltz, H.; Huth, A.; Couelle, C.; England, S.; Love, D.; Davies, K.E.
submitted to the EMBL Data Library, February 1990
A:Reference number: S10346
A:Accession: S10346
A:Molecule type: DNA
A:Residues: 2438-2480 <SPE>
A:Cross-references: UNIPARC:UPI0000173E6E; EMBL:X51934
R:Chamberlain, J.S.; Gibbs, R.A.; Ranier, J.E.; Nguyen, P.N.; Caskey, C.T.
Nucleic Acids Res. 16, 1141-1156, 1988
A>Title: Deletion screening of the Duchenne muscular dystrophy locus via multiplex DNA a
A:Reference number: S02109; MUID:89083552; PMID:3205741
A:Accession: S02243
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 665-722 <CHA>
A:Cross-references: UNIPARC:UPI000001040; EMBL:X13045; NID:g30825; PIDN:CAA31451.1; PID
A:Accession: S02242
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 2098-2146 <CH2>
A:Cross-references: UNIPARC:UPI0000072287; EMBL:X13046; NID:g30827; PIDN:CAA31452.1; PID
A:Accession: S02244
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 2147-2204 <CH3>
A:Cross-references: UNIPARC:UPI000016A837; EMBL:X13048; NID:g30833; PIDN:CAA31454.1; PID
A:Accession: S02109
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 2305-2365; 'K', <CH4>
A:Cross-references: UNIPARC:UPI000016A838; EMBL:X13047; NID:g30831; PIDN:CAA31453.1; PID
R:Günther, I.H.B.; van Paassen, M.H.M.B.; den Dunnen, J.T.; van Ommen, G.G.J.B.
submitted to the EMBL Data Library, March 1992
A:Description: Sequence of Duchenne muscular dystrophy gene exon 60, located directly 5'
A:Reference number: S23736
A:Accession: S23736
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 2980-2995; 'K', 2997-3028 <GIN>
A:Cross-references: UNIPARC:UPI0000173E6F; EMBL:Z11860
R:Heilig, R.; Lemaire, C.; Mandel, J.L.
Nucleic Acids Res. 15, 9129-9142, 1987
A>Title: A 230kb cosmid walk in the Duchenne muscular dystrophy gene: detection of a cor
A:Reference number: S09071; MUID:88067745; PMID:2825128
A:Accession: S09071
A:Molecule type: DNA
A:Residues: 1588-2188 <HET>
A:Cross-references: UNIPARC:UPI0000070802; UNIPARC:UPI0000173E70; EMBL:X06293; EMBL:Y00
A>Note: sequence N-terminal of residue 218 correspond to a putative exon
R:Roberts, R.G.; Coffey, A.J.; Bobrow, M.; Bentley, D.R.

Genomics 16, 536-538, 1993
A>Title: Exon structure of the human dystrophin gene.
A:Reference number: 154186; MUID:93300536; PMID:8314593
A:Accession: 154186
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 984-1411 <RE3>
A:Cross-references: UNIPARC:UPI000007017A; GB:L05642; NID:g181892; PIDN:AAA74506.1; PID:
A:Accession: 168509
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 2850-2979 <ROB>
A:Cross-references: UNIPARC:UPI0000070539; GB:L05649; NID:g181899; PIDN:AAA74508.1; PID:
R:Roberts, R.G.; Coffey, A.D.; Bobrow, M.; Bentley, D.R.
A>Title: Determination of the exon structure of the distal portion of the dystrophin gene
A:Reference number: 154175; MUID:92372062; PMID:1505985
A:Accession: 154175
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 2960-3685 <RES>
A:Cross-references: UNIPARC:UPI000016A860; GB:M66903; NID:g181881; PIDN:AAA35779.1; PID:
R:Rhemprangs, J.; Hillier, M.; Jukes, B.; Floridi, M.; Schwinger, E.; Vobberg, H.P.
Genomics 10, 551-557, 1991
A>Title: Analysis of a dystrophin gene deletion by amplification of mRNA isolated from D
A:Reference number: 154166; MUID:91365360; PMID:1889805
A:Accession: 154166
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 2250-2254 <REA>
A:Cross-references: UNIPARC:UPI000011B804; GB:S54699; NID:g235303; PIDN:AA19754.1; PID:
R:Feener, C.A.; Koenig, M.; Kunkel, L.M.
A>Title: Alternative splicing of human dystrophin mRNA generates isoforms at the carboxy
A:Reference number: 503902; MUID:89181947; PMID:2648158
A:Accession: 503902
A:Molecule type: mRNA
A:Residues: 12-32,3377-3408 <FE8>
A:Cross-references: UNIPARC:UPI000016A859; UNIPARC:UPI000016A861; EMBL:X15148
C:Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the pl
C:Comment: Defects in dystrophin are responsible for the Duchenne/Becker muscular dystro
C:Genetics:
A:Gene: GDB:DM1
A:Cross-references: GDB:119850; OMIM:310200
A:Map position: Xp21.2-Xp21.2
A:Intons: 11/1; 31/3; 62/3; 88/3; 119/3; 177/2; 217/1; 277/3; 320/3; 383/3; 444/2; 494/
3; 3055/1; 3075/2; 3096/1; 3121/1; 3188/2; 3217/1; 3269/3; 3325/2; 3362/3; 3408/2; 3421/
A>Note: The list of introns is incomplete
C:Superfamily: alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat h
C:Keywords: actin binding; alternative splicing; calmodulin binding; cytoskeleton; leuc
elix
F:14-233/Domain: alpha-actinin actin-binding domain homology <ACT>
F:253-337/Region: hinge
F:338-447/Domain: spectrin/dystrophin repeat homology <SP01>
F:448-556/Domain: spectrin/dystrophin repeat homology <SP02>
F:558-667/Domain: spectrin/dystrophin repeat homology <SP03>
F:668-717/Region: hinge
F:718-828/Domain: spectrin/dystrophin repeat homology <SP04>
F:838-934/Domain: spectrin/dystrophin repeat homology <SP05>
F:938-1045/Domain: spectrin/dystrophin repeat homology <SP06>
F:1047-1154/Domain: spectrin/dystrophin repeat homology <SP07>
F:1156-1263/Domain: spectrin/dystrophin repeat homology <SP08>
F:1265-1367/Domain: spectrin/dystrophin repeat homology <SP09>
F:1372-1477/Domain: spectrin/dystrophin repeat homology <SP10>
F:1478-1568/Domain: spectrin/dystrophin repeat homology <SP10>
F:1570-1676/Domain: spectrin/dystrophin repeat homology <SP12>
F:1678-1782/Domain: spectrin/dystrophin repeat homology <SP13>
F:1784-1875/Domain: spectrin/dystrophin repeat homology <SP14>

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F.1876-1982/Domain: spectrin/dystrophin repeat homology <SP15>
F.1984-2101/Domain: spectrin/dystrophin repeat homology <SP16>
F.2103-2208/Domain: spectrin/dystrophin repeat homology <SP17>
F.2210-2316/Domain: spectrin/dystrophin repeat homology <SP18>
F.2327-2423/Domain: spectrin/dystrophin repeat homology <SP19>
F.2424-2470/Domain: hinge
F.2472-2577/Domain: spectrin/dystrophin repeat homology <SP20>
F.2579-2686/Domain: spectrin/dystrophin repeat homology <SP21>
F.2688-2802/Domain: spectrin/dystrophin repeat homology <SP22>
F.2804-2931/Domain: spectrin/dystrophin repeat homology <SP23>
F.2933-3040/Domain: spectrin/dystrophin repeat homology <SP24>
F.3041-3112/Region: hinge
F.3055-3092/Domain: WW repeat homology <WW1>
F.3080-3360/Region: cysteine-rich
F.3506-3527/Region: leucine zipper motif
F.3572-3593/Region: leucine zipper motif

Query Match
Best Local Similarity 5.0%; Score 11; DB 1; Length 3685;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKWN 52
DB 16 VOKKTFTKWN 26

RESULT 18
G02520
plectin - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C:Accession: G02520
R:McLean, W.H.I.; Smith, P.J.D.
submitted to the EMBL Data Library, March 1996
A:Reference number: H01385
A:Accession: G02520
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-4574 <MC>
A:Cross-references: UNIPARC:UPI0000161AF6; EMBL:U53204; NID:q1477645; PIDN:AA05427.1; P
C:Gene: PLEK
C:Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
F.68-283/Domain: alpha-actinin actin-binding domain homology <ACT>

Query Match
Best Local Similarity 5.0%; Score 11; DB 2; Length 4574;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKWN 52
DB 70 VOKKTFTKWN 80

RESULT 19
T13714
kakapo gene protein - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13714; T13715
R:Gregory, S.L.; Brown, N.H.
J. Cell Biol. 143, 1271-1282, 1998
A:Title: Kakapo, a gene required for adhesion between and within cell layers in Drosophila
A:Accession: T13714
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Cross-references: UNIPROT:O77291; UNIPARC:UPI00000840B9; EMBL:AJ011924; NID:g3758908;
A:Accession: T13715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'WM', '77-79', 'SL', '82', 'E', 'WAKDK', '108-109', 'STIQDL', '116-117', 'DR', '138', 'VIRIA', '144

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A/Cross-references: UNIPARC:UPI000020A1A9; EMBL:AJ011925; NID:G3758910; PIDD:CAA09870.1;
C/Genetics:
A/Gene: kak
A/Cross-references: FlyBase:FBgn0013733
A/Note: kak

Query Match 4.5%; Score 10; DB 2; Length 2396;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 OKKFTTKWN 52
|||||
DB 150 OKKFTTKWN 159

RESULT 20
S06461
dyctrophin, brain - rat (fragment)
N/Alternate names: Duchenne muscular dystrophy protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C/Accession: S06461
R/Undel, U.; Zuk, D.; Elnat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe, D.
Nucleotide 337, 76-78, 1989
A/Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain.
A/Reference number: S06461; MUID:89082658; PMID:2909892
A/Accession: S06461
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-98 <NDS>
A/Cross-references: UNIPROT:Q63770; UNIPARC:UPI000017768E; EMBL:X14182
C/Genetics:
A/Introns: 3/1
A/Note: the list of introns may be incomplete
C/Superfamily: dyctrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin
C/Keywords: alternative splicing
F/3-98/Domain: alpha-actinin actin-binding domain homology (fragment) <AAH>

Query Match 4.1%; Score 9; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKW 50
|||||
DB 8 VOKKFTTKW 16

RESULT 21
I39161
dyctonin isoform 2 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Nov-2000
C/Accession: I39161
R/Brown, A.; Dalpe, G.; Mathieu, M.; Kochary, R.
Genomics 29, 777-780, 1995
A/Title: Cloning and characterization of the neural isoforms of human dyctonin.
A/Reference number: I39160; MUID:96121394; PMID:8575775
A/Accession: I39161
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-230 <RES>
A/Cross-references: UNIPARC:UPI000016A21F; EMBL:U31851; NID:G1049105; PIDD:AAC50244.1; F/3-98/Domain: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

Query Match 4.1%; Score 9; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKW 50
|||||
DB 220 VOKKFTTKW 228

RESULT 22
J80233
tropoin-I - scallop (Chlamys nipponensis)

C/Species: Chlamys nipponensis (Japanese scallop)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C/Accession: J80233
R/Tanaka, H.; Ojima, T.; Nishita, K.
J. Biochem. 124, 304-310, 1998
A/Title: Amino acid sequence of tropoin-I from Akazara scallop striated adductor muscle
A/Reference number: J80233; MUID:98351986; PMID:9685719
A/Accession: J80233
A/Molecule type: protein
A/Residues: 1-292 <TAB>
A/Cross-references: UNIPROT:Q7M3Y3; UNIPARC:UPI000017780
C/Superfamily: tropoin I

Query Match 4.1%; Score 9; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RROQEEER 149
|||||
DB 104 RROQEEER 112

RESULT 23
I39160
dyctonin isoform 1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Nov-2000
C/Accession: I39160
R/Brown, A.; Dalpe, G.; Mathieu, M.; Kochary, R.
Genomics 29, 777-780, 1995
A/Title: Cloning and characterization of the neural isoforms of human dyctonin.
A/Reference number: I39160; MUID:96121394; PMID:8575775
A/Accession: I39160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-461 <RES>
A/Cross-references: UNIPARC:UPI000013CB6E; EMBL:U31850; NID:G1049103; PIDD:AAC50243.1; F/3-98/Domain: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

Query Match 4.1%; Score 9; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKW 50
|||||
DB 36 VOKKFTTKW 44

RESULT 24
I49290
dyctonin - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I49290
R/Brown, A.; Bernier, G.; Mathieu, M.; Rosant, J.; Kochary, R.
Nature Genet. 10, 301-306, 1995
A/Title: The mouse dyctonin muscle gene is a neural isoform of bullous pemphigoid an
A/Reference number: I49290; MUID:95400297; PMID:7670468
A/Accession: I49290
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-511 <RES>
A/Cross-references: UNIPROT:Q60824; UNIPARC:UPI000016CB1A; EMBL:U22452; NID:G904018; PIDD:AAC50244.1; F/3-98/Domain: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

Query Match 4.1%; Score 9; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKW 50
|||||
Db 36 VOKKTFTKW 44

RESULT 25

C75120

hypothetical protein PAB1857 - *Pyrococcus abyssi* (strain Orsay)C:Species: *Pyrococcus abyssi*

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: C75120

R:anonymous, Genoscope

A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: C75120

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-602 <KAW>

A:Cross-references: UNIPROT:Q9VOM7; UNIPARC:UPI000006331C; GB:AJ248285; GB:AL096836; NID

A:Experimental source: strain Orsay

A:Genetics:

A:Gene: PAB1857

C:Superfamily: *Pyrococcus horikoshii* hypothetical protein PH1386

Query Match 4.1%; Score 9; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GRPKQLQDE 38
|||||
Db 126 GRPKQLQDE 134

RESULT 26

I49298

dystonin isoform 2 - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000

C:Accession: I49298

R:Brown, A.; Bernier, G.; Mathieu, M.; Rosant, J.; Kothary, R.

Nature Genet. 10, 301-306, 1995

A>Title: The mouse dystonia musculorum gene is a neural isoform of bullous pemphigoid an

A:Reference number: I49290; MUID:95400297; PMID:7670468

A:Accession: I49298

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-686 <RES>

A:Cross-references: UNIPARC:UPI0000028749; EMBL:U25158; NID:g904021; PIDN:AAC52231.1; PI

C:Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

F:209-423/Domain: alpha-actinin actin-binding domain homology <ACT>

Query Match 4.1%; Score 9; DB 2; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKTFTKW 50
|||||
Db 211 VOKKTFTKW 219

RESULT 27

I15570

hypothetical protein C23F12.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: I15570

R:Fullon, B.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C23F12.

A:Reference number: Z18371

A:Accession: I15570

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-874 <FUT>

A:Cross-references: UNIPROT:Q18109; UNIPARC:UPI000007B862; EMBL:U39676; NID:g1049427; P

A:Experimental source: strain Bristol N2; clone C23F12

C:Genetics:

A:Gene: CESP:C23F12.2

A:Map position: X

A:introns: 27/3; 136/3; 240/3; 292/1; 319/1; 346/3; 368/1; 405/3; 421/3; 496/3; 525/3; :

Query Match 4.1%; Score 9; DB 2; Length 874;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GSHDIVDGN 129
|||||
Db 94 GSHDIVDGN 102

RESULT 28

S28381

utrophin - human

N:Alternate names: dystrrophin-related protein

C:Species: *Homo sapiens* (man)

C>Date: 17-Apr-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C:Accession: S28381; S28914; S03966

R:Timney, J.M.

submitted to the EMBL Data Library, November 1992

A:Reference number: S28381

A:Accession: S28381

A:Molecule type: mRNA

A:Residues: 1-3433 <TTN1>

A:Cross-references: UNIPROT:P46939; UNIPARC:UPI00001376CA; EMBL:X69086; NID:g34811; PIDN

R:Timney, J.M.; Blake, D.J.; Roche, A.; Fairbrother, U.; Riss, J.; Byth, B.C.; Knight,

Nature 360, 591-593, 1992

A>Title: Primary structure of dystrrophin-related protein.

A:Reference number: S28914; MUID:93096045; PMID:1461283

A:Accession: S28914

A:Molecule type: mRNA

A:Residues: 27-246; 2839-3443 <TTN2>

A:Cross-references: UNIPARC:UPI0000173E73; UNIPARC:UPI0000173E74; EMBL:X69086

R:Lowe, D.R.; Hill, D.F.; Dickson, G.; Spurr, N.K.; Byth, B.C.; Marsden, R.F.; Walsh, F.

Nature 339, 55-58, 1989

A>Title: An autosomal transcript in skeletal muscle with homology to dystrrophin.

A:Reference number: S03966; MUID:89238543; PMID:2541343

A:Accession: S03966

A:Molecule type: mRNA

A:Residues: 2944-3443 <LOV>

A:Cross-references: UNIPARC:UPI000000673; EMBL:X15488; NID:g30933; PIDN:CA33515.1; PID

C:Comment: This protein is found primarily at the neuromuscular junctions in adult muscul

d regenerating muscle.

C:Genetics:

A:Gene: GDB:UTRN; DMDL

A:Cross-references: GDB:119851; OMIM:128240

A:Map position: 6q24-q24

C:Superfamily: dystrrophin; alpha-actinin actin-binding domain homology; spectrin/dystrp

C:Keywords: actin binding; cytoskeleton; leucine zipper; membrane-associated protein; mu

F:30-248/Domain: alpha-actinin actin-binding domain homology <ACT>

F:308-417/Domain: spectrin/dystrrophin repeat homology <SP01>

F:418-526/Domain: spectrin/dystrrophin repeat homology <SP02>

F:528-637/Domain: spectrin/dystrrophin repeat homology <SP03>

F:638-685/Region: hinge

F:686-796/Domain: spectrin/dystrrophin repeat homology <SP04>

F:804-902/Domain: spectrin/dystrrophin repeat homology <SP05>

F:906-1013/Domain: spectrin/dystrrophin repeat homology <SP06>

F:1015-1122/Domain: spectrin/dystrrophin repeat homology <SP07>

F:1124-1230/Domain: spectrin/dystrrophin repeat homology <SP08>

F:1232-1334/Domain: spectrin/dystrrophin repeat homology <SP09>

F:1336-1450/Domain: spectrin/dystrrophin repeat homology <SP10>

F:1451-1541/Domain: spectrin/dystrrophin repeat homology #status atypical <SP11>

F:1543-1649/Domain: spectrin/dystrrophin repeat homology <SP12>

F:1651-1755/Domain: spectrin/dystrrophin repeat homology <SP13>

F:1856-1973/Domain: spectrin/dystrrophin repeat homology <SP14>

F:1975-2081/Domain: spectrin/dystrophin repeat homology <SP15>
F:2083-2185/Domain: spectrin/dystrophin repeat homology <SP16>
F:2221-2333/Domain: spectrin/dystrophin repeat homology <SP17>
F:2333-2440/Domain: spectrin/dystrophin repeat homology <SP18>
F:2440-2556/Domain: spectrin/dystrophin repeat homology <SP19>
F:2556-2688/Domain: spectrin/dystrophin repeat homology <SP20>
F:2690-2797/Domain: spectrin/dystrophin repeat homology <SP21>
F:2798-2869/Domain: hinge
F:2812-2849/Domain: WW repeat homology <WW1>
F:2837-3117/Region: cytoskeleton-rich
F:3263-3284/Region: leucine zipper motif
F:3328-3349/Region: leucine zipper motif

Query Match 4.1% Score 9; DB 1; Length 3433;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKW 50
DB 32 VOKKFTTKW 40

RESULT 29
S02041
dystrophin, muscle - chicken
N:Alternate names: duchenne muscular dystrophy protein
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: S02041; S02013; S71487
R:Lemaire, C.; Heilig, R.; Mandel, J.L.
Nucleic Acids Res. 16, 11815-11816, 1988
A:Title: Nucleotide sequence of chicken dystrophin cDNA.
A:Reference number: S02041; PMID:89098331; PMID:3062582
A:Accession: S02041
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-3660 <LEM>
A:Cross-references: UNIPROT:P11533; UNIPARC:UPI00001294D5; EMBL:X13369; NID:963369; P1DN
A:Note: 1869-His, 1885-Arg, and sequences lacking 1171-Met were also found
R:Lemaire, C.; Heilig, R.; Mandel, J.L.
EMBL J. 7, 4157-4162, 1988
A:Title: The chicken dystrophin cDNA: striking conservation of the C-terminal coding and
A:Reference number: S02013; PMID:89210800; PMID:3072195
A:Accession: S02013
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-3573, HA, 3576-3660 <LEM2>
A:Cross-references: UNIPARC:UPI0000173E71
R:Heilig, R.; Lemaire, C.; Mandel, J.L.
Nucleic Acids Res. 15, 9129-9142, 1987
A:Title: A 230kb cosmid walk in the Duchenne muscular dystrophy gene: detection of a con
A:Reference number: S09071; PMID:88067745; PMID:2825128
A:Accession: S71487
A:Molecule type: DNA
A:Residues: 222-281 <HE1>
A:Cross-references: UNIPARC:UPI0000173E72
C:Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the pl
C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystro
C:Keywords: actin binding; calmodulin binding; cytoskeleton; leucine zipper; membrane-ae
F:18-237/Domain: alpha-actinin actin-binding domain homology <ACT>
F:253-327/Region: hinge
F:340-449/Domain: spectrin/dystrophin repeat homology <SP01>
F:440-558/Domain: spectrin/dystrophin repeat homology <SP02>
F:560-669/Domain: spectrin/dystrophin repeat homology <SP03>
F:670-719/Region: hinge
F:720-830/Domain: spectrin/dystrophin repeat homology <SP04>
F:838-936/Domain: spectrin/dystrophin repeat homology <SP05>
F:940-1047/Domain: spectrin/dystrophin repeat homology <SP06>
F:1049-1156/Domain: spectrin/dystrophin repeat homology <SP07>
F:1158-1265/Domain: spectrin/dystrophin repeat homology <SP08>
F:1267-1369/Domain: spectrin/dystrophin repeat homology <SP09>
F:1374-1479/Domain: spectrin/dystrophin repeat homology <SP10>

F:1460-1570/Domain: spectrin/dystrophin repeat homology #status atypical <SP11>
F:1572-1678/Domain: spectrin/dystrophin repeat homology <SP12>
F:1680-1784/Domain: spectrin/dystrophin repeat homology <SP13>
F:1787-1877/Domain: spectrin/dystrophin repeat homology #status atypical <SP14>
F:1878-1984/Domain: spectrin/dystrophin repeat homology <SP15>
F:1986-2103/Domain: spectrin/dystrophin repeat homology <SP16>
F:2105-2211/Domain: spectrin/dystrophin repeat homology <SP17>
F:2213-2319/Domain: spectrin/dystrophin repeat homology <SP18>
F:2323-2419/Domain: spectrin/dystrophin repeat homology <SP19>
F:2420-2467/Region: hinge
F:2468-2574/Domain: spectrin/dystrophin repeat homology <SP20>
F:2576-2683/Domain: spectrin/dystrophin repeat homology <SP21>
F:2685-2799/Domain: spectrin/dystrophin repeat homology <SP22>
F:2801-2928/Domain: spectrin/dystrophin repeat homology <SP23>
F:2930-3037/Domain: spectrin/dystrophin repeat homology <SP24>
F:3038-3075/Region: hinge
F:3082-3089/Domain: WW repeat homology <WW1>
F:3079-3357/Region: cytoskeleton-rich
F:3481-3502/Region: leucine zipper motif
F:3547-3568/Region: leucine zipper motif

Query Match 4.1% Score 9; DB 1; Length 3660;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VOKKFTTKW 50
DB 20 VOKKFTTKW 28

RESULT 30
S28916
dystrophin - mouse
N:Alternate names: duchenne muscular dystrophy protein
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S28916; B27162; S10922; C43837; B40134
R:Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.
Nucleic Acids Res. 20, 1725-1731, 1992
A:Title: Human and murine dystrophin mRNA transcripts are differentially expressed durin
A:Reference number: S28916; PMID:92253376; PMID:1579466
A:Accession: S28916
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-3678 <BIE>
A:Cross-references: UNIPROT:P11531; UNIPARC:UPI00000279E7; EMBL:M68859
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R:Koenig, M.; Hoffman, B.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.
Cell 50, 509-517, 1987
A:Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary
A:Reference number: A90897; PMID:87273512; PMID:3607877
A:Accession: B27162
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-201 <MOE>
A:Cross-references: UNIPARC:UPI0000177666
R:Nudel, U.; Zuk, D.; Binat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe, D.
Nature 337, 76-78, 1989
A:Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain.
A:Reference number: S06461; PMID:89082658; PMID:2909892
A:Accession: S10922
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-106 <NUD>
A:Cross-references: UNIPARC:UPI0000177687; EMBL:X14183
R:Rapaport, D.; Lederfein, D.; den Dunnen, J.T.; Grootscholten, P.M.; Van Ommen, G.J.;
Differentiation 49, 187-193, 1992
A:Title: Characterization and cell type distribution of a novel, major transcript of th
A:Reference number: A43837; PMID:92316332; PMID:1377655
A:Accession: C43837
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: WREHLKG, 3069-3181 <RAP>

A:Cross-references: UNIPARC:UPI0000177668
A:Note: sequence extracted from NCBI backbone
R:Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.
Science 238, 347-350, 1987
A:Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.
A:Reference number: A40134; MUID:88018015; PMID:3659917
A:Accession: B40134
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 300-676; 'F', 678-1390 <HOF>
A:Cross-references: UNIPARC:UPI0000177669; GB:M18025
C:Genetics:
A:Introns: 11/1
A:Note: the list of introns may be incomplete
C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin
C:Keywords: actin binding; alternative splicing
F:14-233/Domain: alpha-actinin actin-binding domain homology <ACT>
F:340-449/Domain: spectrin/dystrophin repeat homology <SP1>
F:450-558/Domain: spectrin/dystrophin repeat homology <SP2>
F:2797-2924/Domain: spectrin/dystrophin repeat homology <SP3>
F:3048-3085/Domain: WW repeat homology <WW1>

Query Match
Best Local Similarity 4.1%; Score 9; DB 2; Length 3678;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 YOKKFTKW 50
DB 16 YOKKFTKW 24

RESULT 31
F86242
Unknown protein, 98896-95855 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86242
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86242
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-582 <STO>
A:Cross-references: UNIPROT:O04096; UNIPARC:UPI00000A1725; GB:AE005172; NID:G1931653; PI C:Genetics:
A:Map position: 1

Query Match
Best Local Similarity 3.6%; Score 8; DB 2; Length 592;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 EEEERKR 152
DB 66 EEEERKR 73

RESULT 32
FAHUA2
alpha-actinin 2 - human
C:Species: Homo sapiens (man)
C:Date: 16-Oct-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A40199
R:Beegs, A.H.; Byers, T.J.; Knoll, J.H.M.; Boyce, F.M.; Bruns, G.A.P.; Kunkel, L.M.
J. Biol. Chem. 267, 9281-9288, 1992

A:Title: Cloning and characterization of two human skeletal muscle alpha-actinin genes
A:Reference number: A40199; MUID:92250531; PMID:1339456
A:Accession: A40199
A:Molecule type: mRNA
A:Residues: 1-894 <BEQ>
A:Cross-references: UNIPROT:P35609; UNIPARC:UPI0000125088; GB:M86406; NID:G178053; PIDN C:Comment: The EF hand structures are predicted to be incapable of binding calcium.
C:Comment: The amino-terminal domain is involved in actin binding, the middle domain in ng by the adjacent chain.
C:Genetics:
A:Gene: GDB:ACTN2
A:Cross-references: GDB:127919; OMIM:102573
A:Map position: 1942-1943
C:Complex: homodimer
C:Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin
C:Keywords: actin binding; cardiac muscle; duplication; EF hand; heart; homodimer; skeletal
F:37-250/Domain: alpha-actinin actin-binding domain homology <ACT>
F:280-391/Domain: spectrin/dystrophin repeat homology <SP1>
F:400-506/Domain: spectrin/dystrophin repeat homology <SP2>
F:515-627/Domain: spectrin/dystrophin repeat homology <SP3>
F:636-740/Domain: spectrin/dystrophin repeat homology <SP4>
F:753-785/Domain: calmodulin repeat homology <EF1>
F:789-821/Domain: calmodulin repeat homology <EF2>

Query Match
Best Local Similarity 3.6%; Score 8; DB 1; Length 894;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 SGERLPKP 90
DB 80 SGERLPKP 87

RESULT 33
S02032
alpha-actinin 2, skeletal muscle splice form SK - chicken
C:Species: Gallus gallus (chicken)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S02032; 150604; S36393; S27391; S15481
R:Arimura, C.; Suzuki, T.; Yanagisawa, M.; Imamura, M.; Hamada, Y.; Masaki, T.
Eur. J. Biochem. 177, 649-655, 1988
A:Title: Primary structure of chicken skeletal muscle and fibroblast alpha-actinins deduced
A:Reference number: S02032; MUID:89064821; PMID:3197725
A:Accession: S02032
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-897 <ARI>
A:Cross-references: UNIPROT:P20111; UNIPARC:UPI0000125086; GB:X13874; NID:G63787; PIDN C:Note: part of this sequence was confirmed by protein sequencing
R:Tokune, Y.; Goto, S.; Imamura, M.; Odinata, T.; Kasaki, T.; Endo, T.
Exp. Cell Res. 197, 158-167, 1991
A:Title: Transfection of chicken skeletal muscle alpha-actinin cDNA into nonmuscle and m
A:Reference number: 150604; MUID:92070385; PMID:1720388
A:Accession: 150604
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-897 <TO2>
A:Cross-references: UNIPARC:UPI0000125086; EMBL:X59247; NID:G63030; PIDN:CAA41935.1; PID R:Part, T.
submitted to the EMBL Data Library, October 1992
A:Reference number: S36393
A:Accession: S36393
A:Molecule type: DNA
A:Residues: 662-867 <PAR1>
A:Cross-references: UNIPARC:UPI0000177553; EMBL:X68801
R:Part, T.; Walters, G.T.; Patel, B.; Milla, D.B.; Critchley, D.R.
Eur. J. Biochem. 210, 801-809, 1992
A:Title: A chick skeletal muscle alpha-actinin gene gives rise to two alternatively spliced
A:Reference number: S27391; MUID:93130905; PMID:1483465
A:Accession: S27391
A:Molecule type: DNA
A:Residues: 707-867 <PAR2>
A:Cross-references: UNIPARC:UPI0000177554; EMBL:X68801

A/Note: the authors translated the codon AAA for residue 714 as Leu and AAG for residue 715. The EF hand structures are predicted to be incapable of binding calcium.
C/Comment: The amino-terminal domain is involved in actin binding, the middle domain in actin chain.

C/Genetics: 721/3; 770/3; 792/3; 845/3
A/Introns: 1
A/Note: the list of introns is incomplete
C/Complex: homodimer
C/Superfamily: actin binding; alternative splicing; duplication; EF hand; homodimer; skeletal
C/Keywords: actin binding; alternative splicing; duplication; EF hand; homodimer; skeletal
F/0-253/Domain: alpha-actinin actin-binding domain homology <ACT>
F/83-394/Domain: spectrin/dystrophin repeat homology <SP1>
F/403-509/Domain: spectrin/dystrophin repeat homology <SP2>
F/518-630/Domain: spectrin/dystrophin repeat homology <SP3>
F/639-743/Domain: spectrin/dystrophin repeat homology <SP4>
F/756-788/Domain: calmodulin repeat homology <EF1>
F/792-824/Domain: calmodulin repeat homology <EF2>

Query Match 3.6%; Score 8; DB 2; Length 897;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 SGERLPKP 90
DB 83 SGERLPKP 90

RESULT 34

S45673
alpha-actinin, 115k nonmuscle isoform - chicken
C/Species: Gallus gallus (chicken)
C/Date: 10-Dec-1994 #sequence_rev10 Nov-1995 #text_change 09-Jul-2004
C/Accession: S45673; MUID:94333327; PMID:8055908
R/Imamura, M.; Sakurai, T.; Ogawa, Y.; Ishikawa, T.; Goto, K.; Masaki, T.
Eur. J. Biochem. 223, 395-401, 1994
A/Title: Molecular cloning of low-Ca(2+)-sensitive-type non-muscle alpha-actinin.
A/Reference number: S45673; MUID:94333327; PMID:8055908
A/Accession: S45673
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-904 <IMA>
A/Cross-references: UNIPROT:Q90734; UNIPARC:UPI0000125091; GB:D26597; NID:G517084; PIDN:
J. R. Biol. Chem. 267, 25927-25933, 1992
A/Title: A novel nonmuscle alpha-actinin. Purification and characterization of chicken
A/Reference number: A45090; MUID:93100311; PMID:1334469
A/Accession: A45090
A/Status: preliminary
A/Molecule type: protein
A/Residues: 294-316 <IM2>
A/Cross-references: UNIPARC:UPI00000FBPF
A/Experimental source: lung
A/Note: sequence extracted from NCBI backbone (NCBI:120852)
C/Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re
C/Keywords: actin binding; EF hand
F/42-255/Domain: alpha-actinin actin-binding domain homology <ACT>
F/285-396/Domain: spectrin/dystrophin repeat homology <SP1>
F/403-509/Domain: spectrin/dystrophin repeat homology <SP2>
F/518-630/Domain: spectrin/dystrophin repeat homology <SP3>
F/639-743/Domain: spectrin/dystrophin repeat homology <SP4>
F/756-788/Domain: calmodulin repeat homology <EF1>
F/792-824/Domain: calmodulin repeat homology <EF2>

Query Match 3.6%; Score 8; DB 2; Length 904;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 SGERLPKP 90
DB 83 SGERLPKP 92

RESULT 35

JC7186
alpha-actinin-4 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Mar-2000 #sequence_rev10 Mar-2000 #text_change 09-Jul-2004
C/Accession: JC7186
R/El-Husseini, A.E.D.; Kwanicka, D.; Yamada, T.; Hirohashi, S.; Vincent, S.R.
Biochem. Biophys. Res. Commun. 267, 906-911, 2000
A/Title: BERP, a novel ring finger protein, binds to alpha-actinin-4.
A/Reference number: JC7186; MUID:20139748; PMID:10673389
A/Accession: JC7186
A/Molecule type: mRNA
A/Residues: 1-911 <ELA>
A/Cross-references: UNIPROT:Q9QXQ0; UNIPARC:UPI0000125094; GB:AF190909; NID:G6636118; PI
A/Experimental source: brain
C/Comment: This protein, a calcium-insensitive and nonmuscle form of alpha-actinin impli
finger protein, that acts to anchor microfilaments to various cellular structures.
C/Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re
C/Keywords: brain; EF hand; microfilament

Query Match 3.6%; Score 8; DB 2; Length 911;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 SGERLPKP 90
DB 92 SGERLPKP 99

RESULT 36

T36663
protein kinase, transmembrane - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_rev10 Dec-1999 #text_change 09-Jul-2004
C/Accession: T36663
R/Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A
Submitted to the EMBL Data Library, March 1999
A/Reference number: T21611
A/Accession: T36663
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1089 <SER>
A/Cross-references: UNIPROT:Q9X908; UNIPARC:UPI00000DAF05; EMBL:AL035636; PIDN:CA836479
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCODB:SCS.05C

Query Match 3.6%; Score 8; DB 2; Length 1089;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 EBERRRKR 152
DB 761 EBERRRKR 768

RESULT 37

E84193
chromosome segregation [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_rev10 Feb-2001 #text_change 09-Jul-2004
C/Accession: E84193
R/M, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky,
J.; Leithauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jäbly,
Jung, K.H.; Alam, M.; Freilich, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: E84193
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1190 <STO>
A/Cross-references: UNIPROT:Q9HS95; UNIPARC:UPI00000635B5; GB:AE004437; NID:G10579965;

C/Genetics:
A:Gene: smc1

Query Match 3.6%; Score 8; DB 2; Length 1190;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 LODEREAV 42
|||
Db 768 LODEREAV 775

RESULT 38

A37792

spectrin beta-H chain - fruit fly (*Drosophila melanogaster*) (fragment)

C/Species: *Drosophila melanogaster*
C/Date: 30-Apr-1991 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004

C/Accession: A37792; S70848; S15666

R/Lundbuhl, R.R.; Byers, T.J.; Stewart, C.T.; Kiehart, D.P.

J. Cell Biol. 111, 1849-1858, 1990

A/Title: A beta-spectrin isoform from *Drosophila* (beta-H) is similar in size to vertebrate

A/Reference number: A37792; MUID:91035599; PMID:2229176

A/Accession: A37792

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1645 <DUB>

A/Cross-references: UNIPROT:099140; UNIPARC:UPI000017BD9; GB:X53992

A/Note: Met-14 is the probable initiator

R/Lundbuhl, R.R.

submitted to the EMBL Data Library, July 1990

A/Reference number: S70848

A/Accession: S70848

A/Residues: 1-400,403-410,'QV',411-1645 <DUB>

A/Cross-references: UNIPARC:UPI000008357B; EMBL:X53992; NID:97654; PID:97655

A/Note: Met-14 is the probable initiator

C/Genetics:

A:Gene: FlyBase:Kst

A/Cross-references: FlyBase:FBgn0004167

C/Keywords: actin binding

F/36-258/Domain: alpha-actinin actin-binding domain homology <ACT>

F/288-339/Domain: spectrin/dystrophin repeat homology <SP1>

F/400-510/Domain: spectrin/dystrophin repeat homology <SP2>

F/851-896/Domain: SH3 homology <SH3>

F/999-1091/Domain: spectrin/dystrophin repeat homology <SP3>

F/1303-1408/Domain: spectrin/dystrophin repeat homology <SP4>

F/1409-1512/Domain: spectrin/dystrophin repeat homology <SP5>

Query Match 3.6%; Score 8; DB 2; Length 1645;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 43 OKTFTKX 50
|||
Db 39 OKTFTKX 46

RESULT 39

T42047

insulin receptor homolog - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T42047

R/Knutz, K.D.; Tissenbaum, H.A.; Liu, Y.; Ruvkun, G.

Science 277, 942-945, 1997

A/Title: Daf-2, an insulin receptor-like gene that regulates longevity and diapause in *C.*

A/Reference number: Z22040; MUID:97400619; PMID:9252323

A/Accession: T42047

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1846 <KIM>

A/Cross-references: UNIPROT:O16131; UNIPARC:UPI0000077B82; EMBL:AF012437; NID:92338417; C/Genetics:

A:Gene: daf-2

Query Match 3.6%; Score 8; DB 2; Length 1846;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 123 HDIVDGNH 130
|||
Db 62 HDIVDGNH 69

RESULT 40

A54277

transcription adaptor protein p300 - human

C/Species: *Homo sapiens* (man)

C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C/Accession: A54277; S60344

R/Eckner, R.; Swen, M.E.; Newsome, D.; Gerdes, M.; Decaprio, J.A.; Lawrence, J.B.; Livli

Genes Dev. 8, 869-884, 1994

A/Title: Molecular cloning and functional analysis of the adenovirus E1A-associated 300-

A/Reference number: A54277; MUID:95011587; PMID:7523245

A/Accession: A54277

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-2414 <ECK>

A/Cross-references: UNIPROT:009472; UNIPARC:UPI0000131009; GB:U01877; NID:9495300; PIDN:

A/Note: In the authors' translation 941-Ser is shown after 961 and consequently, residue

R/Lundblad, J.R.; Kwok, R.P.S.; Laurance, M.E.; Harter, M.L.; Goodman, R.H.

Nature 374, 85-88, 1995

A/Title: Adenoviral E1A-associated protein p300 as a functional homologue of the transcr

A/Reference number: S60344; MUID:95174889; PMID:7870179

A/Accession: S60344

A/Status: preliminary

A/Molecule type: protein

A/Residues: 552-660 <LUN>

A/Cross-references: UNIPARC:UPI00001782EB

C/Genetics:

A:Gene: GDB:EP300

A/Cross-references: GDB:9862958; OMIM:502700

A/Map position: 22q13.2-22q13.2

C/Superfamily: transcription coactivator CREB-binding protein; bromodomain homology

C/Keywords: phosphoprotein; transcription; zinc finger

F/1075-1132/Domain: bromodomain homology

F/89,507,1136,1295,1497,1834,1977,2062,2202/Binding site: phosphate (Ser) (covalent) (by

F/1734/Binding site: phosphate (Ser) (covalent) (by protein kinase A) (status predicted

Query Match 3.6%; Score 8; DB 2; Length 2414;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 144 QEEERRR 151
|||
Db 1522 QEEERRR 1529

RESULT 41

T42993

probable spectrin beta chain - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T42993

R/Austin, J.; Pralits, V.; McKown, C.

submitted to the EMBL Data Library, March 1998

A/Description: Sma-I encodes a BH-spectrin homolog required for *C. elegans* morphogenesis

A/Reference number: Z22279

A/Accession: T42993

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-4063 <AUS>

A/Cross-references: UNIPROT:O02425; UNIPARC:UPI0000110113; EMBL:AF053496; PIDN:AAC08577; C/Genetics:

Query Match 3.6%; Score 8; DB 2; Length 4063;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 QKXFTKX 50
|||||
Db 53 QKXFTKX 60

RESULT 42

hypothetical protein R31.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23630; T24242

R/Kershaw, J.
submitted to the EMBL Data Library, November 1996

A/Reference number: Z19774

A/Accession: T23630

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-4101 <WIL>

A/Cross-references: UNIPROT:002425; UNIPARC:UPI000017CF3B; EMBL:Z81570; PIDN:CAB04608.1;
A/Experimental source: clone K12G11

R/Lennard, N.
submitted to the EMBL Data Library, July 1996

A/Reference number: Z19862

A/Accession: T24242

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-4101 <W12>

A/Cross-references: UNIPARC:UPI000017CF3B; EMBL:Z75956; PIDN:CAB00130.1; GSPDB:GN00023;
A/Experimental source: clone R31

C/Genetics:

A/Map position: 5

A/Introm: 29/3; 89/3; 184/3; 312/3; 812/2; 1461/3; 1531/3; 2050/2; 2413/2; 2466/2; 3008

Query Match 3.6%; Score 8; DB 2; Length 4101;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 QKXFTKX 50
|||||
Db 75 QKXFTKX 82

RESULT 43

165646
Duchenne muscular dystrophy protein - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C/Accession: I65646

R/Cnelly, U.; Gligenkranz, H.; Lambert, M.; Hamard, G.; Chafey, P.; Recan, D.; Katz, P.
Cell 63, 1239-1248, 1990

A/Title: Effect of dystrophin gene deletions on mRNA levels and processing in Duchenne's
A/Reference number: I52806; MUID:91084852; PMID:2261642

A/Accession: I65646

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-125 <RES>

A/Cross-references: UNIPROT:Q14174; UNIPARC:UPI000007156E; GB:M63075; NID:G181591; PIDN:
C/Genetics:

A/Map position: 1

A/Cross-references: GDB:119850; OMIM:310200

A/Map position: Xp21.2-Xp21.2

C/Species: Mus musculus
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C/Accession: T49719

R/Schulte, U.; Altmann, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000

OY 124 DIVDGNH 130
|||||
Db 61 DIVDGNH 67

RESULT 44

hypothetical protein YUL124c - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein J0714

C/Species: Saccharomyces cerevisiae
C/Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C/Accession: S56905

R/Ciepluch, C.; Kordey, E.; Pujol, A.; Jauniaux, J.C.
submitted to the Protein Sequence Database, September 1995

A/Reference number: S56891

A/Accession: S56905

A/Molecule type: DNA

A/Residues: 1-172 <CZ1>

A/Cross-references: UNIPROT:P47017; UNIPARC:UPI0000530D0; EMBL:Z49399; NID:G1008119; PI

C/Genetics:

A/Map position: 10L

A/Status: preliminary

A/Reference number: S56891

A/Accession: S56905

A/Molecule type: DNA

A/Residues: 1-172 <CZ1>

A/Cross-references: UNIPROT:P47017; UNIPARC:UPI0000530D0; EMBL:Z49399; NID:G1008119; PI

C/Genetics:

A/Map position: 10L

A/Status: preliminary

A/Reference number: S56891

A/Accession: S56905

A/Molecule type: DNA

A/Residues: 1-172 <CZ1>

A/Cross-references: UNIPROT:Q9HSW4; UNIPARC:UPI0000063526; GB:AE004437; NID:G10579698; I

C/Genetics:

A/Map position: 1

A/Cross-references: GDB:119850; OMIM:310200

A/Map position: Xp21.2-Xp21.2

C/Species: Mus musculus

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C/Accession: T49719

R/Schulte, U.; Altmann, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000

Query Match 3.2%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 LRDGRML 75
|||||
Db 58 LRDGRML 64

RESULT 45

B84165
glucose-1-phosphate thymidyltransferase [imported] - Halobacterium sp. NRC-1

C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B84165

R/Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laeky, S.
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A/Title: Genome sequence of Halobacterium species NRC-1

A/Reference number: B84160; MUID:20504483; PMID:11016950

A/Accession: B84165

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-218 <STO>

A/Cross-references: UNIPROT:Q9HSW4; UNIPARC:UPI0000063526; GB:AE004437; NID:G10579698; I

C/Genetics:

A/Map position: 1

A/Cross-references: GDB:119850; OMIM:310200

A/Map position: Xp21.2-Xp21.2

C/Species: Mus musculus

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C/Accession: T49719

R/Schulte, U.; Altmann, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000

Query Match 3.2%; Score 7; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 VRRQGE 146
|||||
Db 92 VRRQGE 98

RESULT 46

hypothetical protein B2121.320 [imported] - Neurospora crassa

C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C/Accession: T49719

R/Schulte, U.; Altmann, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000

A/Reference number: 225022
A/Accession: T49719
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-226 <SCH>
A/Cross-references: UNIPARC:UPI0000179D83; EMBL:AL356172; GSPDB:GN00116; NCSP:B23121.320
A/Experimental source: BAC clone B23121; strain OR74A
C/Genetics:
A/Gene: NCSP:B23121.320
A/Intron: 90/1
C/Superfamily: Neurospora crassa hypothetical protein B23121.320

Query Match 3.2%; Score 7; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 146 EERRRR 152
38 EERRRR 44

RESULT 47
AB0957
conserved hypothetical protein STY3934 [imported] - *Salmonella enterica* subsp. *enterica*
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A/Note: this species has also been called *Salmonella typhi*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AB0957
R/Packhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AB0957
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-251 <PAR>
A/Cross-references: UNIPARC:UPI000005A692; GB:AL513382; PIDN:CAD03150.1; PID:q16504785;
C/Genetics:
A/Gene: STY3934

Query Match 3.2%; Score 7; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MELORTS 7
103 MELORTS 109

RESULT 48
F69844
conserved hypothetical protein yjbn - *Bacillus subtilis*
C/Species: *Bacillus subtilis*
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C/Accession: F69844
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertei, C.; Bron, S.D.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Geller, K.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.; Koether, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Luthers, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet, M.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.; Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: F69844
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-266 <KUN>
A/Cross-references: UNIPROT:O31612; UNIPARC:UPI000006021B; GB:Z99110; GB:AL009126; NID:5
A/Experimental source: strain 168
C/Genetics:
A/Gene: yjbn
C/Superfamily: ATP-NAD(H) kinase

Query Match 3.2%; Score 7; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 174 SKGDQVS 180
7 SKGDQVS 13

RESULT 49
G97246
aacC-type DNA-binding domain-containing protein, transcription regulator [imported] - *Clostridium acetobutylicum*
C/Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: G97246
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G97246
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-279 <KUN>
A/Cross-references: UNIPROT:O97FC2; UNIPARC:UPI00000CA649; GB:AE001437; PIDN:AAK80762.1;
A/Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A/Gene: CAC2818

Query Match 3.2%; Score 7; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 114 RVHLENM 120
160 RVHLENM 166

RESULT 50
G86155
hypothetical protein T14P4.13 [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: G86155
R/Thelander, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.; W. Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Moore, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: G86155
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-290 <STO>
A/Cross-references: UNIPROT:Q9FMX9; UNIPARC:UPI00000A60B7; GB:AE005172; NID:g9972379; PI
C/Genetics:

A:Map position: 1

Query Match 3.2%; Score 7; DB 2; Length 290;

Best Local Similarity 100.0%; Pred. No. 51; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 144 QEEERK 150

Db 219 QEEERK 225

Search completed: March 4, 2006, 07:10:34
Job time : 72 secs